

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: April 14, 2000, 18:27:02 ; Search time 1381.26 Seconds
(without alignments)
-3066.588 Million cell updates/sec

Title: US-09-388-090-3
Perfect score: 1395
Sequence: 1 ggtttcaaaaatccata.....tcaggccaatggccgtcaa 1395

Scoring table:	OLIGO_NUC	Gapop 60.0 , Gapext 60.0	Score	Query Match No.	Length	DB ID	Description
Searched:	821193 seqs,	-1518192014 residues		c 1	23	1.6	Z72082 P.gambiae s
Word size :	0	Total number of hits satisfying chosen Parameters: 1642386		c 2	23	1.6	Z72084 A.gambiae s
Database :	GenEmbl:*	Minimum DB seq length: 0		c 3	20	1.4	U72352 Gallus gallus
	1: gb_bai:*	Maximum DB seq length: 1000000		c 4	20	1.4	X62210 G.oxydans g
	2: gb_bai:*	Post-processing: Listing first 1000 summaries		c 5	20	1.4	AC013843 Drosophila
	3: gb_om:*			c 6	20	1.4	AC005052 Homo sapiens
	4: qb_ov:*			c 7	19	1.4	X16660 Human HTLV-1
	5: qb_pat:*			c 8	19	1.4	AF072440 Enterobacter
	6: qb_ph:*			c 9	19	1.4	AF067430 Mus musculus
	7: qb_pil:*			c 10	19	1.4	U50199 Caenorhabditis elegans
	8: qb_pil2:*			c 11	19	1.4	Z97211 S.pombe chromosome
	9: qb_pr1:*			c 12	19	1.4	AB016875 Arabidopsis thaliana
	10: qb_pr2:*			c 13	19	1.4	AC002415 Homo sapiens
	11: qb_pr3:*			c 14	18	1.3	M62465 Mouse thrombopoietin receptor
	12: qb_ro:*			c 15	18	1.3	G14673 human STS
	13: qb_sts:*			c 16	18	1.3	AB011872 Unidentifed protein
	14: qb_sy:*			c 17	18	1.3	X73519 Human species b
	15: qb_un:*			c 18	18	1.3	M24213 Herpesvirus
	16: qb_vl:*			c 19	18	1.3	U83277 Giardia intestinalis
	17: em_fun:*			c 20	18	1.3	D78602 Arribidopsis thaliana
	18: em_hum1:*			c 21	18	1.3	Y12467 D.rerio mRNA
	19: em_hum2:*			c 22	18	1.3	U96451 Danio rerio mRNA
	20: em_in:*			c 23	18	1.3	AF087654 Mus musculus mRNA
	21: em_om:*			c 24	18	1.3	U14732 Tribolium castaneum mRNA
	22: em_or:*			c 25	18	1.3	AF188715 Caenorhabditis elegans mRNA
	23: em_ov:*			c 26	18	1.3	U67369 Human growth hormone mRNA
	24: em_pat:*			c 27	18	1.3	M60853 Chicken thymidine kinase mRNA
	25: em_ph:*			c 28	18	1.3	M87276 Mouse thrombopoietin receptor mRNA
	26: em_pl:*			c 29	18	1.3	X95538 M.intracellularis mRNA
	27: em_ro:*			c 30	18	1.3	AC005895 Homo sapiens mRNA
	28: em_sts:*			c 31	18	1.3	Z33502 H.influenzae mRNA
	29: em_sy:*			c 32	18	1.3	AJ224959 Thauera australis mRNA
	30: em_un:*			c 33	18	1.3	AE000263 Escherichia coli mRNA
	31: em_vl:*			c 34	18	1.3	U79580 Pseudomonas aeruginosa mRNA
	32: qb_htg1:*			c 35	18	1.3	AC015001 Drosophilaelegans mRNA
	33: qb_htg2:*			c 36	18	1.3	AE000729 Aquifex aeolicus mRNA
	34: qb_lini:*			c 37	18	1.3	U46844 Mycobacterium tuberculosis mRNA
	35: qb_in2:*			c 38	18	1.3	AD000012 Mycobacterium leprae mRNA
	36: em_ba1:*			c 39	18	1.3	AC000396 Genomic DNA
	37: em_ba2:*			c 40	18	1.3	AC000502 Homo sapiens genomic DNA
	38: em_ba3:*			c 41	18	1.3	ZL133218 Streptomyces coelicolor A3(2) genomic DNA
	39: em_hum4:*			c 42	18	1.3	AC005239 Homo sapiens genomic DNA
	40: qb_pr4:*			c 43	18	1.3	AC011540 Homo sapiens genomic DNA
	41: qb_htg3:*			c 44	18	1.3	U23515 Caenorhabditis elegans genomic DNA
	42: qb_htg4:*			c 51	18	1.3	AC009588 Homo sapiens genomic DNA
	43: qb_htg5:*			c 52	18	1.3	AC006090 *** SEQDB
				c 53	18	1.3	AC01673 Homo sapiens genomic DNA
				c 54	18	1.3	AC016473 Homo sapiens genomic DNA
				c 55	18	1.3	AC016415 Homo sapiens genomic DNA
				c 56	18	1.3	Continuation (4 of 4)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

57	1.3	73009	8	ATAC007069	c	130	17	1.2	5907	1	ECSAPABCD		
58	1.3	74901	35	AC005444	c	131	17	1.2	6057	1	AB01757		
59	1.3	83859	7	AB024038	c	132	17	1.2	6191	2	RPU7364		
c	60	1.3	100793	11	AF070717	Homo sapi	133	17	1.2	6597	9	HSCAN	
c	61	1.3	120391	45	AC017146	Drosophil	134	17	1.2	6642	9	HUMORF10	
c	62	1.3	124469	41	AC008347	Drosophil	135	17	1.2	6704	2	STREPCOMY	
c	63	1.3	129441	32	HSAC002099	Homo sapi	136	17	1.2	6738	2	AF116907	
c	64	1.3	132353	33	AC002355	Homo sapi	137	17	1.2	6824	6	AF112470	
c	65	1.3	137658	10	HS10211	Human DNA	138	17	1.2	10477	2	AE0170754	
c	66	1.3	152355	11	AC005668	Homo sapi	139	17	1.2	10477	2	AE000227	
c	67	1.3	156187	44	AC013593	Homo sapi	140	17	1.2	11342	1	AE003044	
c	68	1.3	157066	42	AC010436	Homo sapi	141	17	1.2	11344	40	AF044611	
c	69	1.3	160437	43	AC011984	Homo sapi	142	17	1.2	11978	2	AE001955	
c	70	1.3	165942	10	HS1054A22	Human DNA	143	17	1.2	12298	16	AF02448	
c	71	1.3	168765	11	CNS01DFF	BAC sequence	144	17	1.2	12457	12	AB01543	
c	72	1.3	168835	11	HS652LB	Human DNA	145	17	1.2	12653	12	D87521	
c	73	1.3	177865	42	AC008525	Homo sapi	146	17	1.2	12653	12	Mus musculu	
c	74	1.3	177726	41	AC004083	Homo sapi	147	17	1.2	13857	2	AE000185	
c	75	1.3	177328	44	AC007289	Drosophil	148	17	1.2	15009	43	AC04599	
c	76	1.3	18007	35	AC007257	Drosophil	149	17	1.2	15141	16	SH1R0IE	
c	77	1.3	185116	11	AC005823	Homo sapi	150	17	1.2	16231	12	RNPBCT	
c	78	1.3	205540	11	AC002324	Homo sapi	151	17	1.2	16578	1	D90721	
c	79	1.3	210296	33	HS1057B20	Homo sapi	152	17	1.2	17769	1	D90757	
c	80	1.3	212118	43	AC009244	Homo sapi	153	17	1.2	18399	41	AC030652	
c	81	1.3	310565	32	CEY62FS	Caenorhabdi	154	17	1.2	19196	1	D90738	
c	82	1.3	330250	40	AF049895	Homo sapi	155	17	1.2	20252	2	AF029714	
c	83	1.3	337565	32	CEY72D3	Drosophil	156	17	1.2	22449	1	SPSN426	
c	84	1.3	377411	11	AF099426	Zea mays	157	17	1.2	22449	1	SPSN426	
c	85	1.3	378378	9	MMU13387	Mus muscu	158	17	1.2	24754	41	AC008674	
c	86	1.3	3803C10	9	HS303C10	H.sapiens t	159	17	1.2	28762	34	CE26376	
c	87	1.3	39513	13	G45126	G45126 Z1/Z74-1 Ze	160	17	1.2	30000	16	BHY30KB	
c	88	1.3	407257	35	MTPS16SR	X99173 Petrocephal	161	17	1.2	30352	1	MTCY109	
c	89	1.3	412080	12	MPB32533	U33533 Petrocephal	162	17	1.2	31896	45	AC077879	
c	90	1.3	413377	11	CEY12D3	Z98665 Caenorhabdi	163	17	1.2	32591	34	CEFF6D3	
c	91	1.3	417129	8	AF099426	AF099426 IDIR agent	164	17	1.2	32591	34	CEFF6D3	
c	92	1.3	417135	12	MMU13387	Mus muscu	165	17	1.2	33359	1	U01159	
c	93	1.3	417142	9	HS19PT009	A005191 Mus muscu	166	17	1.2	33384	41	AC08915	
c	94	1.3	417159	7	CALIPASB	AF020760 Homo sapi	167	17	1.2	34584	34	CET7C5	
c	95	1.3	417160	12	FILTRAU	AF0175324 Mus muscu	168	17	1.2	34877	41	AC030408	
c	96	1.3	417165	11	BLTHYBL	AF0175324 Mus muscu	169	17	1.2	34877	41	AC031324	
c	97	1.3	417220	8	AF079296	Melica cu	170	17	1.2	35637	7	SPCC74	
c	98	1.3	417230	3	DOBGBALL	L223429 Canis beta-	171	17	1.2	37881	34	CELOK9H9	
c	99	1.3	417242	9	HS19PT009	296436 H.sapiens t	172	17	1.2	40739	6	AF115103	
c	100	1.3	417247	10	CALIPASB	AF020760 Homo sapi	173	17	1.2	41052	11	AC024499	
c	101	1.3	417250	12	GGVITRO	Y11030 G.gallus mR	174	17	1.2	41055	1	SC6G1	
c	102	1.3	417254	12	ROTIDIR9	AF0175324 Mus muscu	175	17	1.2	41084	10	AC02500	
c	103	1.3	417255	3	BOTUROPLX	LJ19542 Bovine urop	176	17	1.2	41324	1	MSGY109	
c	104	1.3	417256	9	HUMELFAII	AM117412 Homo sapi	177	17	1.2	41552	34	CEC17D12	
c	105	1.3	417257	16	BIMSEPC	D30655 Homo sapi	178	17	1.2	41716	43	AC014073	
c	106	1.3	417258	12	AF010760	L4129 Bovine immu	179	17	1.2	42800	41	AC010288	
c	107	1.3	417259	7	RNTENFA	S79942 EIF4A2-prot	180	17	1.2	43084	34	CEKF5	
c	108	1.3	417260	12	AF0175324	298952 Calymperes	181	17	1.2	44993	43	AC014424	
c	109	1.3	417261	10	AF0175324	298956 Dicranum sc	182	17	1.2	49377	5	188042	
c	110	1.3	417262	9	AF0175324	GG072394 Gallus gall	183	17	1.2	50714	35	AC005471	
c	111	1.3	417263	8	AF042275	AF042275 Oryza sat	184	17	1.2	52298	42	AC014073	
c	112	1.3	417264	10	AF010325	22829 S.cerevisia	185	17	1.2	52359	41	AC005954	
c	113	1.3	417265	12	AF010326	X68264 H.sapiens M	186	17	1.2	53517	32	AC02405	
c	114	1.3	417266	7	D87895	AF010326 Dr.rosophil	187	17	1.2	56033	43	AC015690	
c	115	1.3	417267	35	AF010328	X84210 R.norvegicus	188	17	1.2	66489	44	AC016267	
c	116	1.3	417268	35	AF114486	AF010327 Dr.rosophil	189	17	1.2	67747	42	AC012630	
c	117	1.3	417269	35	AF010325	AF010325 Dr.rosophil	190	17	1.2	70932	10	AP000269	
c	118	1.3	417270	12	X84209 R.norvegicus	X84209 R.norvegicus	191	17	1.2	77118	43	AC015954	
c	119	1.3	417271	12	AF010326	AF010326 Dr.rosophil	192	17	1.2	77201	45	AC007307	
c	120	1.3	417272	12	AF010328	D87895 Aspergillus	193	17	1.2	78583	41	AC009709	
c	121	1.3	417273	40	AF010328	AF010328 Dr.rosophil	194	17	1.2	78583	44	AC009709	
c	122	1.3	417274	35	AF114486	AF010327 Dr.rosophil	195	17	1.2	80470	44	AC015678	
c	123	1.3	417275	9	HSU09607	U9607 Human JAK f	196	17	1.2	82011	41	AC009667	
c	124	1.3	417276	9	AB014587	AB014587 Homo sapi	197	17	1.2	82692	20	AC03924	
c	125	1.3	417277	12	AF055586	AF055586 Vibrio ch	198	17	1.2	82957	7	AB01476	
c	126	1.3	417278	4864	9	HSCMRP	X96395 H.sapiens m	199	17	1.2	83083	44	AC013671
c	127	1.3	417279	16	SH1SEQ	M81222 Herpesvirus	200	17	1.2	83572	8	AC00508	
c	128	1.3	417280	11	HSSMA2S1	U78726 Homo sapien	201	17	1.2	85420	40	AC004672	
c	129	1.3	417281	12	PDOOXABCD	X78196 P.denitrifi	202	17	1.2	85943	41	AC009472	

203	17	1.2	86212	7	AB010074	Arabidopsis	AC009456	Homo sapi	AC009456	41	1.2	177316	17
c 204	17	1.2	87960	45	AC017906	AC017906 Drosophil	AC013285	Homo sapi	AC013285	32	1.2	179482	17
c 205	17	1.2	88401	8	F23M19	AC007454 Arabidops	AC010977	Homo sapi	AC010977	44	1.2	181564	17
c 206	17	1.2	88035	8	F15M1	AC006577 Sequence	AC010739	Homo sapi	AC010739	44	1.2	183687	17
c 207	17	1.2	89765	45	AC017970	AC017970 Drosophil	AF079317	Sphingomo	AF079317	2	1.2	184457	17
c 208	17	1.2	91019	35	AC008105	AC008105 Drosophil	AC011028	Homo sapi	AC011028	44	1.2	185792	17
c 209	17	1.2	91421	33	AC008105	AC008105 Homo sapi	AL133323	Homo sapi	AL133323	33	1.2	186594	17
c 210	17	1.2	93216	11	AC003016	AC003016 Human BAC	AC011191	Homo sapi	AC011191	42	1.2	186557	17
c 211	17	1.2	94281	1	AP00042	AP000342 Plasmid R	AC011851	Homo sapi	AC011851	42	1.2	187886	17
c 212	17	1.2	96964	33	AC004906	AC004906 Homo sapi	AC005041	Homo sapi	AC005041	42	1.2	188014	17
c 213	17	1.2	97487	41	AC011433	AC011433 Homo sapi	AC012149	Homo sapi	AC012149	40	1.2	190014	7
c 214	17	1.2	97542	43	AF202964	AF202964 Homo sapi	AC005035	Homo sapi	AC005035	40	1.2	190545	7
c 215	17	1.2	97854	45	AC017411	AC017411 Drosophil	AC008177	Homo sapi	AC008177	42	1.2	190814	7
c 216	17	1.2	98524	40	AF188025	AF188025 Homo sapi	AC005894	Drosophil	AC005894	42	1.2	190814	7
c 217	17	1.2	100000	10	AP000032	AP000032 Homo sapi	AC013285	Homo sapi	AC013285	42	1.2	193556	17
c 218	17	1.2	100000	10	AP000033	AP000033 Homo sapi	AC013285	Homo sapi	AC013285	43	1.2	196337	17
c 219	17	1.2	100000	10	AP000179	AP000179 Homo sapi	AC013285	Homo sapi	AC013285	43	1.2	198303	17
c 220	17	1.2	100656	32	CEY20056	Z98859 Caenorhabdi	AC007147	Drosophil	AC007147	44	1.2	198283	17
c 221	17	1.2	1005325	11	HS614C15	AL035250 Human DNA	297337	Arabidopsis	297343 Arabidopsis	40	1.2	193708	17
c 222	17	1.2	105607	43	AC013410	AC013410 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 223	17	1.2	106926	40	AF042089	AF042089 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 224	17	1.2	109016	8	ATP10K17	ATP10K17 Continuation (2 of	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 225	17	1.2	110000	32	CEY14H9_1	AC00348 Economic S	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 226	17	1.2	111390	8	AC00348	AC00348 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 227	17	1.2	116215	11	AC004130	AC004130 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 228	17	1.2	116490	32	HS018914	AL021392 Human DNA	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 229	17	1.2	120206	11	HS439F8	AC010580 Drosophil	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 230	17	1.2	121121	41	AC010580	AC007150 Drosophil	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 231	17	1.2	121474	41	AC007150	AC008209 Drosophil	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 232	17	1.2	123872	33	AC008209	AC007099 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 233	17	1.2	125032	40	AC007099	AC008186 Drosophil	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 234	17	1.2	125237	33	AC008186	AC008186 Drosophil	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 235	17	1.2	125534	41	AC008750	AC008750 Human DNA	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 236	17	1.2	126813	41	AF165423	AF165423 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 237	17	1.2	127596	42	AF165177	AF165177 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 238	17	1.2	128320	11	HS3114	Z99943 Human DNA S	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 239	17	1.2	130532	41	AC006519	AC006519 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 240	17	1.2	135237	33	AC008186	AC008186 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 241	17	1.2	136386	42	AC01138	AC01138 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 242	17	1.2	138445	33	AC002979	AC002979 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 243	17	1.2	139328	35	AC006302	AC006302 Drosophil	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 244	17	1.2	140524	43	AC015869	AC015869 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 245	17	1.2	134365	41	AC006119	AC006119 Bovine he	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 246	17	1.2	135051	16	BHV1CCEN	AC004801 Bovine he	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 247	17	1.2	136386	42	AC01138	AC01138 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 248	17	1.2	148432	35	AC004642	AC004642 Drosophil	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 249	17	1.2	149572	11	AC004695	AC004695 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 250	17	1.2	149645	41	AC011510	AC011510 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 251	17	1.2	150299	11	HS019L4	AL022724 Human DNA	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 252	17	1.2	150915	32	HSDD368B9	D90910 Syncerocyst	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 253	17	1.2	148126	42	AC007284	AC007284 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 254	17	1.2	154614	12	MM573K1	AC004649 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 255	17	1.2	155176	11	HS453P22	AC012743 Drosophil	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 256	17	1.2	160310	45	AC007311	AC007311 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 263	17	1.2	155811	33	AC015821	AC015821 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 264	17	1.2	156362	35	AC006472	AC006472 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 265	17	1.2	158173	43	AC013270	AC013270 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 266	17	1.2	158412	40	AC005334	AC005334 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 267	17	1.2	159580	41	AC011432	AC011432 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 268	17	1.2	160304	45	AC007404	AC007404 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 269	17	1.2	160735	44	AC015821	AC015821 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 270	17	1.2	163616	43	AC013276	AC013276 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 271	17	1.2	164554	40	AC007687	AC007687 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 272	17	1.2	164901	10	HS10883	AC013394 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 273	17	1.2	165604	44	AC013394	AC013394 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 274	17	1.2	173810	32	HS030M6	AC005863 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 275	17	1.2	174050	44	AC009863	AC009863 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8
c 276	17	1.2	174755	33	AC005805	AC005805 Homo sapi	297343	Arabidopsis	297343 Arabidopsis	40	1.2	197674	8

349	16	918	24	E11731	c	422	16	1.1	CP98955	Ceratodon p
		951	1	PFU19743	c	423	16	1.1	SAZ98558	Schistidium
		951	1	PSEOPRH	c	424	16	1.1	1933	L07613
		951	1	U2102 Pseudomonas	c	425	16	1.1	1958	Pseudomonas
		962	2	AFL17965	c	426	16	1.1	1968	Z98557
		973	16	AFL102782	c	427	16	1.1	1983	Pottia trun
		981	2	AFL117969	c	428	16	1.1	AF181634	Drosophil
		1000	7	LETFT5	c	429	16	1.1	2004	M37888
		1004	3	BTCNP1	c	430	16	1.1	2026	Staphylococ
		1018	12	RATCPS113	c	431	16	1.1	4	GGU47276
		1041	2	AF044794	c	432	16	1.1	2061	E. coli xer
		1047	2	AF090797	c	433	16	1.1	5	E08061
		1054	10	BCY15704	c	434	16	1.1	5	DNA encodin
		1065	10	AF007782	c	435	16	1.1	123834	Sequence 9
		1071	1	NGU75635	c	436	16	1.1	143345	Pseudomonas
		1071	1	M12335	c	437	16	1.1	144694	Sequence 5
		1071	1	Rat nucleus	c	438	16	1.1	14694	Sequence 5
		1071	1	Neisseria	c	439	16	1.1	AF18888	Musca dom
		1103	12	AY242803	c	440	16	1.1	17332	D. dictyonotus
		1103	12	Sporobolu	c	441	16	1.1	17332	E. coli xer
		1105	9	D78265	c	442	16	1.1	17332	DNA encodin
		1105	9	Mus musculu	c	443	16	1.1	17334	Human mRNA
		1122	1	X89851	c	444	16	1.1	AF078107	Homo sapi
		1122	1	H. sapiens D	c	445	16	1.1	AR054117	Sequence
		1125	1	X53316	c	446	16	1.1	1230	S. typhimurium
		1125	1	S. typhimurium	c	447	16	1.1	5	HSRRNNA
		1125	12	D50591	c	448	16	1.1	2157	X. laevigata
		1126	12	PAPYCP	c	449	16	1.1	2157	Human mRNA
		1126	12	RNCPSIX38	c	450	16	1.1	2157	Streptomyces
		1148	5	E12704	c	451	16	1.1	2157	Y. enterocolitica
		1151	7	PCU17117	c	452	16	1.1	2157	Y. enterocolitica
		1152	34	AB010284	c	453	16	1.1	2157	Y. enterocolitica
		1279	4	AB022601	c	454	16	1.1	2157	Y. enterocolitica
		1287	12	STLEB	c	455	16	1.1	2157	Y. enterocolitica
		1288	4	MUSCIPFC	c	456	16	1.1	2157	Y. enterocolitica
		1288	4	XLETFIAI	c	457	16	1.1	2157	Y. enterocolitica
		1288	5	I14303	c	458	16	1.1	2157	Y. enterocolitica
		1300	1	STU20795	c	459	16	1.1	2157	Y. enterocolitica
		1320	2	RMU51475	c	460	16	1.1	2157	Y. enterocolitica
		1348	2	ESU13036	c	461	16	1.1	2157	Y. enterocolitica
		1351	16	AF120270	c	462	16	1.1	2157	Y. enterocolitica
		1357	35	MSU11879	c	463	16	1.1	2157	Y. enterocolitica
		1364	34	MOTP4A	c	464	16	1.1	2157	Y. enterocolitica
		1375	1	PEP1658R19	c	465	16	1.1	2157	Y. enterocolitica
		1401	1	ESRIBRNA1	c	466	16	1.1	2157	Y. enterocolitica
		1401	35	CPU43545	c	467	16	1.1	2157	Y. enterocolitica
		1421	34	MSLMTER6A	c	468	16	1.1	2157	Y. enterocolitica
		1436	1	P29P3P4	c	469	16	1.1	2157	Y. enterocolitica
		1440	4	SSAJ664	c	470	16	1.1	2157	Y. enterocolitica
		1440	4	SSAJ665	c	471	16	1.1	2157	Y. enterocolitica
		1475	2	PSU33309	c	472	16	1.1	2157	Y. enterocolitica
		1476	1	PSU33313	c	473	16	1.1	2157	Y. enterocolitica
		1479	1	DNEPS335	c	474	16	1.1	2157	Y. enterocolitica
		1479	5	AR038196	c	475	16	1.1	2157	Y. enterocolitica
		1479	5	I44026	c	476	16	1.1	2157	Y. enterocolitica
		1479	5	I44026	c	477	16	1.1	2157	Y. enterocolitica
		1479	5	I49035	c	478	16	1.1	2157	Y. enterocolitica
		1480	4	SSAJ665	c	479	16	1.1	2157	Y. enterocolitica
		1533	35	AF132170	c	480	16	1.1	2157	Y. enterocolitica
		1534	34	TCSBTB	c	481	16	1.1	2157	Y. enterocolitica
		1542	7	CROEE3	c	482	16	1.1	2157	Y. enterocolitica
		1561	16	I44026	c	483	16	1.1	2157	Y. enterocolitica
		1600	4	XLETFIAII	c	484	16	1.1	2157	Y. enterocolitica
		1601	1	AF092910	c	485	16	1.1	2157	Y. enterocolitica
		1620	40	HUMS651NB	c	486	16	1.1	2157	Y. enterocolitica
		1656	7	BLYRCAB	c	487	16	1.1	2157	Y. enterocolitica
		1662	12	CPO238589	c	488	16	1.1	2157	Y. enterocolitica
		1674	34	DROSJETGF	c	489	16	1.1	2157	Y. enterocolitica
		1679	4	AF001299	c	490	16	1.1	2157	Y. enterocolitica
		1694	34	BMJ00916	c	491	16	1.1	2157	Y. enterocolitica
		1695	1	MSGY414B	c	492	16	1.1	2157	Y. enterocolitica
		1720	12	RNU55276	c	493	16	1.1	2157	Y. enterocolitica
		1722	16	LCVY16308	c	494	16	1.1	2157	Y. enterocolitica
		1728	1	HUMHPSA	c	495	16	1.1	2157	Y. enterocolitica
		1738	3	AF076281	c	496	16	1.1	2157	Y. enterocolitica
		1758	1	PAAMP	c	497	16	1.1	2157	Y. enterocolitica
		1760	16	AF063220	c	498	16	1.1	2157	Y. enterocolitica
		1763	16	AF063221	c	499	16	1.1	2157	Y. enterocolitica
		1791	34	AB013012	c	500	16	1.1	2157	Y. enterocolitica
		1811	12	STPEPMG	c	501	16	1.1	2157	Y. enterocolitica
		1840	35	XANPELY	c	502	16	1.1	2157	Y. enterocolitica
		1845	1	D89826	c	503	16	1.1	2157	Y. enterocolitica
		1857	1	D89826	c	504	16	1.1	2157	Y. enterocolitica
		1871	12	MMU36274	c	505	16	1.1	2157	Y. enterocolitica
					c	422	16	1.1	CP98955	Ceratodon p
					c	423	16	1.1	SAZ98558	Schistidium
					c	424	16	1.1	1933	L07613
					c	425	16	1.1	1958	Pseudomonas
					c	426	16	1.1	1968	Z98557
					c	427	16	1.1	1983	Pottia trun
					c	428	16	1.1	2004	AF181634
					c	429	16	1.1	2026	GGU47276
					c	430	16	1.1	2061	E. coli xer
					c	431	16	1.1	2061	DNA encodin
					c	432	16	1.1	2061	Sequence 9
					c	433	16	1.1	2061	Sequence 5
					c	434	16	1.1	2076	AF18888
					c	435	16	1.1	2090	Musca dom
					c	436	16	1.1	2107	DDIAC732
					c	437	16	1.1	2108	D50914
					c	438	16	1.1	2108	Human mRNA
					c	439	16	1.1	2130	AF078107
					c	440	16	1.1	2130	Homo sapi
					c	441	16	1.1	2157	AR054117
					c	442	16	1.1	2169	HSRRNNA
					c	443	16	1.1	2169	AJ132236
					c	444	16	1.1	2195	ECCOBBD
					c	445	16	1.1	2224	AF243607
					c	446	16	1.1	2224	DMEPEPAR
					c	447	16	1.1	2224	D87842
					c	448	16	1.1	2245	STGYQR
					c	449	16	1.1	2245	NMU79481
					c	450	16	1.1	2245	Bacillus m
					c	451	16	1.1	2245	PRVNBBCTP
					c	452	16	1.1	2508	CBU5326
					c	453	16	1.1	2508	RNUDENAGE
					c	454	16	1.1	2508	DM2E23599
					c	455	16	1.1	2531	BMCGSM
					c	456	16	1.1	2670	CECBQ1
					c	457	16	1.1	2683	1. X. campestri
					c	458	16	1.1	2692	X. campestris
					c	459	16	1.1	2798	RICPR1
					c	460	16	1.1	2812	ECOSNLPD
					c	461	16	1.1	2812	ECOSNLPD
					c	462	16	1.1	2812	ECOSNLPD
					c	463	16	1.1	2812	ECOSNLPD
					c	464	16	1.1	2831	SSQACREP
					c	465	16	1.1	2838	ECOGLFDA
					c	466	16	1.1	2847	D00425
					c	467	16	1.1	2936	ECPBPX
					c	468	16	1.1	2936	AF180367
					c	469	16	1.1	2960	PRVNAB
					c	470	16	1.1	2962	CRUT356
					c	471	16	1.1	3204	AF047363
					c	472	16	1.1	3204	Paenibaci
					c	473	16	1.1	3219	Y17898
					c	474	16	1.1	321	

641	27602	34	CET01C1	Z68010	Caenorhabdi	7114
642	16	1.1	28618	34	CEY37H9A	c 7115
643	16	1.1	29624	35	CELB0545	c 7116
644	16	1.1	30034	8	OSD0541	c 7117
645	16	1.1	30148	34	CFEP57C7	c 7118
646	16	1.1	30419	35	CELT07H8	c 7119
647	16	1.1	30941	1	SC4656	c 7200
648	16	1.1	31312	10	AP000283	c 7201
649	16	1.1	31638	1	RMEXPGN5	c 7202
650	16	1.1	31795	34	CELT07H6	c 7203
651	16	1.1	31913	43	AC013216	c 7204
652	16	1.1	31975	8	SPCC553	c 7205
653	16	1.1	32239	1	SCTA1	c 7206
654	16	1.1	32105	10	AP000284	c 7207
655	16	1.1	32195	20	AC004154	c 7208
656	16	1.1	32266	34	CSXY947B	c 7209
657	16	1.1	32806	32	HS5819C10	c 7300
658	16	1.1	33500	11	AC03004	c 7301
659	16	1.1	33896	35	CELT05AB	c 7302
660	16	1.1	33930	34	CEK04H4	c 7303
661	16	1.1	33954	7	SC9305	c 7304
662	16	1.1	34083	2	AFT24757	c 7305
663	16	1.1	34150	1	MTCY190	c 7306
664	16	1.1	34238	32	CEY4F10-4	c 7307
665	16	1.1	34774	43	AC013899	c 7308
666	16	1.1	34860	34	CELR173	c 7309
667	16	1.1	35292	1	MTCY3C7	c 7310
668	16	1.1	35294	43	AC013816	c 7401
669	16	1.1	35559	6	PABY13918	c 7402
670	16	1.1	35580	6	AB00550	c 7403
671	16	1.1	35737	11	AC005263	c 7404
672	16	1.1	35743	34	CELF31E8	c 7405
673	16	1.1	35769	8	SPAC23A1	c 7406
674	16	1.1	36360	1	MTV20B11	c 7407
675	16	1.1	36615	43	AC014144	c 7408
676	16	1.1	37186	1	MSGT244	c 7409
677	16	1.1	37218	11	HSN11D4	c 7500
678	16	1.1	37225	34	CEC17E4	c 7501
679	16	1.1	37307	10	HS33SH7	c 7502
680	16	1.1	37394	8	SPAC2F3	c 7503
681	16	1.1	37439	34	CEP35E2	c 7504
682	16	1.1	37462	43	AC013090	c 7505
683	16	1.1	37700	35	CEHL14E04	c 7506
684	16	1.1	37693	10	AP000522	c 7507
685	16	1.1	37821	1	MLCB1770	c 7508
686	16	1.1	38558	8	SPBC21B10	c 7509
687	16	1.1	38563	34	CEN20B3	c 7510
688	16	1.1	38715	11	AC00092	c 7511
689	16	1.1	39146	10	CHI9R28051	c 7602
690	16	1.1	39480	34	CFC34C6	c 7603
691	16	1.1	39752	35	CELC04F5	c 7604
692	16	1.1	39839	43	AC013000	c 7605
693	16	1.1	40018	7	AP000740	c 7606
694	16	1.1	40162	40	USS675	c 7607
695	16	1.1	40210	43	SPCC135	c 7608
696	16	1.1	40337	7	SC9559	c 7609
697	16	1.1	40442	2	SC18	c 7610
698	16	1.1	40665	35	CELC27F2	c 7701
699	16	1.1	40665	35	CELC27F5	c 7702
700	16	1.1	40880	42	AC012633	c 7703
701	16	1.1	40965	42	AC012633	c 7704
702	16	1.1	41099	32	CEY94AT	c 7705
703	16	1.1	41037	45	AC01776	c 7706
704	16	1.1	41071	34	CELB0303	c 7707
705	16	1.1	41397	34	CEB0285	c 7708
706	16	1.1	41594	41	AC010964	c 7709
707	16	1.1	41525	1	SCH24	c 7710
708	16	1.1	41625	10	HSS171R	c 7711
709	16	1.1	41848	33	AC006098	c 7712
710	16	1.1	41906	1	SC5C7	c 7713
711	16	1.1	42282	34	CELB0304	c 7714
712	16	1.1	42418	32	HS38G	c 7715
713	16	1.1	42660	34	CEP15D3	c 7716

c 787	16	1.1	73491	43	AC009641	Homo sapi	AP000109	10	100000	1.1	100000	10	AP000109
c 788	16	1.1	73635	50	ATAC011915	Arabidopsis	AP000131	10	100000	1.1	100000	10	AP000131
c 789	16	1.1	73739	35	AC001646	Drosophila	AC001646	862	16	1.1	100000	10	AP000153
c 790	16	1.1	74780	33	AC005445	Drosophila	AC005445	862	16	1.1	100000	10	AP000185
c 791	16	1.1	75079	43	AC015047	Drosophila	AC015047	863	16	1.1	100000	10	AP000209
c 792	16	1.1	75263	41	AC009835	Homo sapi	AC009835	864	16	1.1	100201	4.1	AC008366
c 793	16	1.1	75263	41	AC009835	Homo sapi	AC009835	865	16	1.1	100354	4.0	AC007590
c 794	16	1.1	76743	35	AC005473	Drosophila	AC005473	866	16	1.1	100509	4.2	AC010123
c 795	16	1.1	77618	45	AC017050	Homo sapi	AC017050	867	16	1.1	101340	4.5	AC018104
c 796	16	1.1	78189	44	AC015737	Homo sapi	AC015737	868	16	1.1	102004	8	ATAC005395
c 797	16	1.1	78205	43	AC015748	Homo sapi	AC015748	869	16	1.1	102739	11	HS671014
c 798	16	1.1	78505	33	AC006408	Homo sapi	AC006408	870	16	1.1	103370	4.1	AC003352
c 799	16	1.1	79109	7	AB016871	Arabidopsis	AB016871	871	16	1.1	103632	8	AF074021
c 800	16	1.1	79114	33	AC005475	Drosophila	AC005475	872	16	1.1	104059	4.2	AC010110
c 801	16	1.1	79227	10	HS148E12	Human DNA	AL008725	873	16	1.1	104081	11	HS021263J07
c 802	16	1.1	79528	11	HS466N1	Human DNA	2977630	874	16	1.1	104130	4.5	AC017069
c 803	16	1.1	79706	42	AC009746	Drosophila	AC009746	875	16	1.1	104153	5.0	AC010155
c 804	16	1.1	79740	42	AC009945	Drosophila	AC009945	876	16	1.1	105126	4.3	AC01428
c 805	16	1.1	80000	46	AC005652	** SEQUE	AC005652	877	16	1.1	105320	3.2	AP000668
c 806	16	1.1	80389	35	AC005663	Drosophila	AC005663	878	16	1.1	105788	3.2	AP000749
c 807	16	1.1	80393	7	AB003032	Arabidopsis	AB003032	879	16	1.1	105809	4.3	AC013758
c 808	16	1.1	80446	35	AC004288	Drosophila	AC004288	880	16	1.1	105816	4.5	AC017069
c 809	16	1.1	80818	42	AC009746	Drosophila	AC009746	881	16	1.1	106273	11	HS71018A4
c 810	16	1.1	81487	11	HS7770223	Human DNA	AL118509	882	16	1.1	106723	4.2	AC010064
c 811	16	1.1	81786	11	AC003002	Human DNA	AC003002	883	16	1.1	106953	3.3	AC006982
c 812	16	1.1	82359	40	AC004942	Homo sapi	AC004942	884	16	1.1	108879	11	AC004804
c 813	16	1.1	82503	7	AB016886	Arabidopsis	AB016886	885	16	1.1	109076	4.6	AC000796
c 814	16	1.1	83253	7	AP000383	Arabidopsis	AP000383	886	16	1.1	109566	3.3	AC0077803
c 815	16	1.1	83605	43	AC014193	Drosophila	AC014193	887	16	1.1	109826	3.3	AC008311
c 816	16	1.1	83693	8	ATT13J8	Arabidopsis	AL0035524	888	16	1.1	110000	3.2	CEY5C10_0
c 817	16	1.1	83922	8	T9A4	Drosophila	AF096373	889	16	1.1	110000	3.2	CEY116A8_2
c 818	16	1.1	84246	34	AC002512	Drosophila	AC002512	890	16	1.1	110000	3.2	CEY37H9_0
c 819	16	1.1	84305	41	AC006943	Mus muscu	AC006943	891	16	1.1	110000	3.2	CEY41H9_1
c 820	16	1.1	84323	10	HS138BB7	Human DNA	2987752	892	16	1.1	110000	3.2	CEY7TH9_3
c 821	16	1.1	85561	8	ATAC009126	Arabidopsis	AC009346	893	16	1.1	110000	3.2	CEY8HC10_1
c 822	16	1.1	85674	40	AF164343	Homo sapi	AF164343	894	16	1.1	110000	3.2	CEY5C10_0
c 823	16	1.1	85740	43	AC014942	Drosophila	AC014942	895	16	1.1	110000	3.2	CEY33C10_1
c 824	16	1.1	86643	42	AC012311	Homo sapi	AC012311	896	16	1.1	110000	3.2	CEY55C10_3
c 825	16	1.1	86699	7	F21H2	Drosophila	AC009050	897	16	1.1	110000	3.2	CEY7F8_1
c 826	16	1.1	87077	40	HUAC004097	Human Chr	AC004097	898	16	1.1	110000	3.2	CEY8LG3_2
c 827	16	1.1	87210	7	AB011485	Arabidopsis	AB011485	899	16	1.1	110000	3.3	AC007194_1
c 828	16	1.1	88178	44	AC011187	Homo sapi	AC011187	900	16	1.1	110000	4.1	AP008691_1
c 829	16	1.1	88413	8	ATAC005724	Arabidopsis	AC005724	901	16	1.1	110000	4.1	AC011455_0
c 830	16	1.1	88512	8	F21H2	Drosophila	AC078434	902	16	1.1	110926	4.1	AC009846
c 831	16	1.1	89016	10	HS118B21	Human DNA	AL109633	903	16	1.1	111723	11	HS113341
c 832	16	1.1	89448	40	AC005067	Homo sapi	AC005067	904	16	1.1	113220	4.2	AC006015
c 833	16	1.1	91311	43	AC000105	Drosophila	AC000105	905	16	1.1	112074	9	AP000112
c 834	16	1.1	91813	42	AC010716	Drosophila	AC010716	906	16	1.1	112710	3.2	CEY36D014
c 835	16	1.1	91863	8	ATAC004667	Drosophila	AC004667	907	16	1.1	112710	4.2	AC011252
c 836	16	1.1	92472	10	HS181C9	Human DNA	AL109624	908	16	1.1	112753	4.1	AC009459
c 837	16	1.1	92948	8	ATAF000657	Arabidopsis	ATAF000657	909	16	1.1	115118	10	AP000247
c 838	16	1.1	93131	43	AC000105	Homo sapi	AC000105	910	16	1.1	113220	4.2	AF022962
c 839	16	1.1	93659	42	AC009377	Drosophila	AC009377	911	16	1.1	113637	4.1	AC009368
c 840	16	1.1	93845	8	ATAC004684	Homo sapi	AC004684	912	16	1.1	116387	4.0	AC005301
c 841	16	1.1	94386	11	HS452M16	Drosophila	AC044493	913	16	1.1	114567	4.1	AC009417
c 842	16	1.1	96400	11	HS633020	Human DNA	AL102310	914	16	1.1	115118	10	AP000247
c 843	16	1.1	96679	8	ATT8P19	Drosophila	AT133315	915	16	1.1	115119	4.3	HS163M9
c 844	16	1.1	96801	8	ATAC003333	Arabidopsis	AC003033	916	16	1.1	115962	4.1	AC008441
c 845	16	1.1	96924	45	AC017831	Drosophila	AC017831	917	16	1.1	116828	3.2	AL109826
c 846	16	1.1	96953	42	AC011428	Homo sapi	AC011428	918	16	1.1	116858	4.2	AC010029
c 847	16	1.1	97146	8	ATTC16L1	Drosophila	AC007259	919	16	1.1	114567	4.1	AC010750
c 848	16	1.1	97308	43	AC013925	Drosophila	AC013925	920	16	1.1	117696	4.2	AC012192
c 849	16	1.1	97693	40	AC002313	Homo sapi	AC002313	921	16	1.1	118067	10	HS163M9
c 850	16	1.1	98052	10	AP00219	Drosophila	AC00219	922	16	1.1	118100	4.5	AC012911
c 851	16	1.1	98052	10	AP003031	Homo sapi	AP003031	923	16	1.1	118235	12	AC003060
c 852	16	1.1	98124	8	ATTC16L1	Drosophila	AC00341	924	16	1.1	118831	11	HS188311
c 853	16	1.1	98695	35	AC005556	Drosophila	AC005556	925	16	1.1	119001	8	ATF9D16
c 854	16	1.1	99384	8	AF076243	Arabidopsis	AF076243	926	16	1.1	119122	4.2	AC005896
c 855	16	1.1	99416	8	AC009398	Genomic S	AC009398	927	16	1.1	119348	4.2	AC009369
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c 857	16	1.1	100000	9	AB020860	Homo sapi	AB020860	929	16	1.1	119755	3.3	AC007755
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c 936	16	1.1	12337	41	AF189001	Homo sapi			
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c 939	16	1.1	125010	41	AC011394	Homo sapi			
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c 941	16	1.1	125568	42	AC008239	Homo sapi			
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c 946	16	1.1	127528	33	AC007831	Drosophil			
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c 949	16	1.1	128598	1	D00912	Synechocystis sp. PCC6803			
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c 954	16	1.1	129238	41	AC011469	Homo sapi			
c 955	16	1.1	129779	35	AC006214	Drosophil			
c 956	16	1.1	130142	45	AC017890	Homo sapi			
c 957	16	1.1	130536	44	AC007807	Drosophil			
c 958	16	1.1	130583	41	AC007420	Drosophil			
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c 978	16	1.1	137654	32	AP000713	Homo sapi			
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c 991	16	1.1	143852	8	AF161269	Oryza sativa			
c 992	16	1.1	143131	33	AC007039	Homo sapi			
c 993	16	1.1	143774	32	HSP1023				
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c 995	16	1.1	144720	41	AC009177	Drosophil			
c 996	16	1.1	145531	42	AC011180	Homo sapi			
c 997	16	1.1	146153	35	AC007452	Drosophil			
c 998	16	1.1	146458	33	AL133290	Homo sapi			
c 999	16	1.1	144497	33	AC007718	Homo sapi			
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ALIGNMENTS

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VERSION									
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Anopheles gambiae.									
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;									
Pterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anopheles.									
REFERENCE									
1 (bases 1 to 91)									
AUTHORS									
Zheng L., Benedict,M.Q., Cornel,A.J., Collins,F.H. and Kafatos,F.C.									
TITLE									
An integrated genetic map of the African human malaria vector									
mosquito.									
mosquitoes.									
Genetics 143 (1996) In press									
JOURNAL									
European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, FRG									
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AUTHORS									
Zheng L.									
JOURNAL									
Submitted (23-APR-1996) Zheng L., European Molecular Biology									
Laboratory, Meyerhofstrasse 1, 69117 He									

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FEATURES source CDS mutation BASE COUNT ORIGIN	GOGDH LOCUS G.oxydans gdh gene. DEFINITION X62710 S60040 ACCESSION X62710.1 VERSION GI:58416 KEYWORDS coenzyme PQQ; gdh gene; gluconic acid dehydrogenase; quinoprotein. Glucobacter oxydans. Glucobacter oxydans Bacteria; Proteobacteria; alpha subd.; Glucobacter. REFERENCE 1 (bases 1 to 2890) AUTHORS Cleton-Jansen,A.M., Dekker,S., van de TITLE A single amino acid substitution char of quinoprotein glucose dehydrogenase in <i>Glucobacter oxydans</i> JOURNAL Mol. Gen. Genet. 229 (2), 206-212 (1991) MEDLINE 92017653 REFERENCE 2 (bases 1 to 2890) AUTHORS Goosen,N. TITLE Direct Submission JOURNAL Submitted (07-FEB-1992) N. Goosen, Dept. of Mol. Genetics, Gorlaeus Laboratories, Leiden University, P O Box 9502, 2300 RA Leiden, THE NETHERLANDS Location/Qualifiers 1. 2890 /organism="Glucobacter oxydans" /db_xref="taxon:442" FEATURES source RBS gene CDS /codon_start=1 /trans_table=11 /product="Glucose dehydrogenase (pyrroloquinoline-quinone)" /protein_id="CA444594." /db_xref="GI:4433391." /db_xref="SWISS-PROT:P22177." /translation"MTISRPRIWALIAVAFALCGAIIYGGAWAAIGGPIIYVIL GIALLATAFLSPRRNPAIYLAVVYGTAVIWLTVGLDIALIPRSDIVLGIVL LIPPEVSPARSVARGRPRCRSPAVYVNLASFLPHDPSGELQIANSAPDPO NPASENHAYGRDAGDRWSPLNQINATVNLKVWHIHDMMMNDPGATNEAT PFLIEENHAPTDCAKDSLIPVNLSDVYDADIGKTCKWYEDFNGKRN QVEPTSPVITDKLILANSATDNGSYKQKOSAEGATQDVYKWTWYD PDQWGSDFTRKDSERAPGVAL NADTGKLAWEFYOTVHDLMELPSGDTLQVPAIYPTGIDFLVDRR TKEIVVRAPEFTVPOGAAPGDTSTPQMSLVDLQVPAIYPTGIDFLVDRR MDSDGNPAPTDCAKDSLIPVNLSDVYDADIGKTCKWYEDFNGKRN QVEPTSPVITDKLILANSATDNGSYKQKOSAEGATQDVYKWTWYD PDQWGSDFTRKDSERAPGVAL NADTGKLAWEFYOTVHDLMELPSGDTLQVPAIYPTGIDFLVDRR TKEIVVRAPEFTVPOGAAPGDTSTPQMSLVDLQVPAIYPTGIDFLVDRR YFTLRLREGPFTPSLKSLIPFGDGMFENGGLADPQRYAFANPISLPLFYSQVLP RGFPNPLPMEENAKGTGGGGTLDGSMYSSLPLIPPPKIGMPCRIPPG VAGIDLKNUKVWORNRNLSLDPVLLPGLVPSLUGGPLSTAGNUGLF SMOYIRAYNLITGKVLWQDRLPAGQRATPTIYAKNGKQIVTYAGGHNNSFPTRMGDD IIYAYVRAPEFTVPOGAAPGDTSTPQMSLVDLQVPAIYPTGIDFLVDRR 293. 654 /gene="gdh" /note="membrane spanning fragment" 2612 /gene="gdh" /note="mutation changing substrate specificity"	2890 bp DNA
Query Match Best Local Similarity 100.0%; Pred. No. 11; Matches 20; Conservative 0; Mismatches 0; Gaps 0; Query 817 ggcatcttcgtccatccc 836 Db 814 GGATCTCCCTTGCATGCC 833	Query Match Best Local Similarity 100.0%; Pred. No. 11; Matches 20; Conservative 0; Mismatches 0; Gaps 0; Query 597 atggggcgctgcattggcg 616 Db 340 ATGGGGCGCTGCATGCC 359	Query Match Best Local Similarity 1.4%; Score 20; DB 4; Length 1435; Mutation BASE COUNT ORIGIN

RESULT 5 AC013843/C LOCUS HTG 16-NOV-1999 DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces
ACCESSION AC013843 VERSION GI:6437492
KEYWORD HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Muscomorpha; Neoptera; Endopterygota; Diptera; Brachycera;
Eukaryota; Neoptera; Ephydriidea; Drosophilidae; Drosophila.
1 (bases 1 to 31427)
Adams,M. and Venter,J.C.
Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10211866 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
1. .31427
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 8828 a 6834 c 6605 g 9160 t
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 344 aaggaaaggcaggatgacggc 363
Db 6506 AGAAAGAAGCAGATGACGGC 6487
RESULT 6 AC005052 LOCUS HTG 12-JUN-1998 DEFINITION Homosapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unorderd pieces.
ACCESSION AC005052
VERSION GI:3212939
KEYWORD HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 144734)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 144734)
Waterston,R.H.
Direct Submission
JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT * NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1. 12549 * 12565: gap of unknown length
* 12566 66999: contig of 54434 bp in length
* 67000 67016: gap of unknown length
* 67017 144734: contig of 77718 bp in length.
FEATURES SOURCE 1. .144734
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/db_xref="taxon:3606"
/clie="RG038K21"
BASE COUNT 37015 a 34072 c 33954 g 39639 t 34 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 673 agctgcgccaaacgaaacta 692
Db 84680 AGCTGTGCCAACGAAAGCTA 84699
RESULT 7 HTLV1RES LOCUS HTLV1RES 2153 bp DNA PRI 24-JUN-1998 DEFINITION Human HTLV-1 related endogenous retroviral sequence (HRES-1/1).
ACCESSION X16660.1 VERSION GI:3256208
KEYWORDS endogenous retrovirus; long terminal repeat.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2153)
AUTHORS Perl,A.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-1989) Perl A., Roswell Park Memorial Institute, 666 Elm Street, Buffalo, NY 14263, USA
REMARK revised by [3]
REFERENCE 2 (bases 1 to 2153)
AUTHORS Perl,A., Rosenblatt,J.D., Chen,I.S., Divincenzo,J.P., Bever,R., Poless,B.J. and Abraham,G.N.
TITLE Detection and cloning of new HTLV-related endogenous sequences in man
JOURNAL Nucleic Acids Res. 17 (17), 6841-6854 (1989)
MEDLINE 8938640
REFERENCE 3 (bases 1 to 2153)
AUTHORS Perl,A.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-1998) Perl A., Roswell Park Memorial Institute, 666 Elm Street, Buffalo, NY 14263, USA
COMMENT On Jun 26, 1998 this sequence version replaced 91:38034.
Data kindly reviewed (08-JAN-1990) by Perl A.
FEATURES SOURCE 1. .2153
/organism="Homo sapiens"
/db_xref="taxon:3606"
/cell_type="T lymphocyte"
/cell_line="MA-T"
/clone_lib="lambda DASH"
/clone="HRES-1/1"
310. .994
/note="putative retroviral"
repeat_unit 310. .313
/note="A"
/rpt_type=INVERTED
misc_feature 463. .470
/note="TAR sequence (trans-activation region)"
TATA_signal 782. .788
misc_feature 839. .844
/note="putative"
repeat_unit 990. .993
/note="A"

gene 18470..21495 "T14F9_3"
 CDS join(18470..18568,18613..18739,18793..18964..1907
 19421..19633..19677..19907..19952..20127..20175..20435,
 20477..20599..21300..21495)
 /gene="T14F9_3"
 /note="coded for by C. elegans cDNA ykt9c7..3; coded for by
 L. elegans homolog; similar to beta hexosaminidase
 gene"

/gene="T14F9.1"				
/note="coded for by C. elegans CDNA yk89e9.5; coded for by C. elegans CDNA cm795; coded for by C. elegans CDNA yk5295.5; coded for by C. elegans CDNA yk765.5; coded for by C. elegans CDNA yk87d8.5; coded for by C. elegans CDNA yk131f1.5; coded for by C. elegans CDNA yk76e-3; coded for by C. elegans CDNA yk8d8.3; coded for by C. elegans CDNA yk5295.3; coded for by C. elegans CDNA yk131f1.3; similar to S. cerevisiae vacuolar H ⁽⁺⁾ -ATPase 54 kd subunit (sp:R41807)"				
/codon_start=1				
/protein_id="AAH91366.1"				
/db_xref="GI:121313557"				
/translation="MAEVPHNTPAVDMLNATSRLEAQELNRNPWNWSYFRSOMI DQDDYNTITFENAKNSKEERDQVLAANNNGQAQMTMANLITQVARDQNYVRLTMDI DMHQDKSKRVELFHAAAROKRTTQYQLGQRDNFIVQMSSTIAKLAFCGTTRM EGQDQGYFFSEFLKEOLKNSTNDYANTTARCLQMLMRHDYEFDSGQVLTVALN QVTKNFQLOLQOLIFAWWCJFNADIAKAPASIGLQLOAGDILSESTEKFVTRILLASF NGVNLISKYRDREVKEPQEAQVYQCKTLLTTELMDAKYDPLEDDYKFLTEBLTSLSYH DLSSDEYYSEVRSGRLQWSPVHKSEKFWRNASKENDQFEEVKLILKLLESSHDDPL ILCVASHDIDGEVPRKIVVEQIQGKAAYMRLLTAEPDNVRYHALAVOKLMVHNH WEYLGIQDSDYQDTDVAK"				
BASE COUNT	11140	a	7051	c
ORIGIN	6678	g	11810	t
Query Match	1.4%	Score 19;	DB 34;	Length 36679;
Best Local Similarity	100.0%	Pred. No. 42;		
Matches	19;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps
			0;	0
QY	619	cccttcgggttggacaaca	637	
Db	31265	CCCTCGGCTTGCAACA	31284	
RESULT	11			
SPBC2F12	SPBC2F12	38012 bp	DNA	PLN
LOCUS	S.pombe chromosome II	cosmid	c2F12.	23-NOV-1999
DEFINITION				
ACCESSION	297211	GI:6273683		
VERSION	297211.2	GI:6273683		
KEYWORDS	60S ribosomal protein L22; atf crab-family transcription factor; by2; b2IP; bZIP; transcription factor; ceg1; cell cycle regulation; ergosterol; synthase; Homo D box; IMP dehydrogenase; inosine-5'-monophosphate dehydrogenase; kinesin-like; L2; L8; leucine zipper; mitochondrial 60S ribosomal protein L17; mitotic cell cycle start; mrna capping enzyme; mrna guanylyltransferase; rep2; rpk3; rpk5b; rpk5c; rp117; rp18-2; serine rich; serine threonine protein kinase; transcriptional activator; zinc finger C2H2 type yeast.			
SOURCE	schizosaccharomyces pombe			
ORGANISM	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.			
AUTHORS	Wood, V., Rajandream, M.A., Barrell, B.G., Skelton, J. and Churcher, C.M.			
TITLE	Direct Submission			
JOURNAL	Submitted (27-JUN-1997) European Schizosaccharomyces genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk			
REFERENCE	The Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA			
AUTHORS	On Nov 7, 1999 this sequence version replaced gi:2239231.			
COMMENT	Notes: Details of yeast sequencing at the Sanger Centre are available on the World Wide Web. (URL: http://www.sanger.ac.uk/Projects/S_pombe/) During 1995 to 1996 about 80% of S. pombe chromosome 1 was sequenced by the Sanger Centre. The sequencing of the S. pombe genome is now being continued with funding from The European Commission. Fourteen European laboratories, including			

the Sanger Centre, are participating in the project.

Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in pombase (an ACEDB database) with additional predictions for the branch/acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.

CDS are numbered using the following system eg SPBC23H2.01c, SP (S. pombe), B (Chromosome 2), c25H2 (cosmid name), .01 (first CDS), C (complementary strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid c2F12 is overlapped at the 5' end by cosmid c19C2 and at the 3' end by cosmid c1D7

FEATURES /source

/organism="Schizosaccharomyces pombe"

/strain="972h-"

/db_xref="taxon:4896"

/chromosome="II"

/map="IIR"

/clone="cosmid c2F12"

/note="nominal overlap with cosmid SPBC19C2, EM:AU109731

S.pombe chromosome 2"

complement(1..371)

/gene="SPBC2F12.16"

/partial

/join(1..308,359..371)

/note="SPBC2F12.16"

/note="SPBC2F12.16, similarity: to C elegans

O17040, T15B7.2, PROTEIN, (271 aa), fasta scores, opt.:135,

E():2.7e-06, (.36 .88 identity in 87 aa overlap)"

/codon_start=1

/label="SPBC2F12.16

/product="hypothetical protein"

/protein_id="CAB10163.2"

/db_xref="SWISS-PROT:014346"

/translation="MSKILKIOYLKLNYNTSCFLWMSVLLRGLIWGTITKDATVVFHE

YNTLYRWVQTLIAAEVHSIFGGLYSSSPLTTIQQASRLYLVWGYCPFSYVIEGSPI

YLSMI"

complement(309..327)

/gene="SPBC2F12.16"

/note="tttacaaatggtaaaaatag, splice branch and acceptor"

/partial

/join(1008..2069)

/note="gttaga, splice donor sequence"

gene

/gene="SPBC2F12.15c"

/join(1008..1235..1308..2069)

/label="SPBC2F12.15c"

/product="hypothetical protein"

/protein_id="CAB10162.1"

/db_xref="IC,I:2239244"

/swiss-prot="014345"

/translation="UNLHKYSTQCQCVLYLAKYCMOTIALS1MSGVOWLANYIKI

NKNRVGLIILFYLIVTVCVLTNTTPGSSPSENSEDPNSTRQMTLQNGSRCEKC

QEYKCDRSHCISQCNKCIERMDHHKPFECYLADSYCLVYST

FVAIKTFTTAEGANTSAYIVWGLTFAPAGMSVUMTATTYFUTSLIHLNNTLES

SSWSRSRYTHSTQPNVNGWYENWCQIMGKSPFLWLPPNSIGEVYEPNANALP

QTEEKNNDKLYKSSVPASSIAGAEGMSSDDEEQYAMKNRNRNPHMGOEWIEDFLY"

1236..1241

/gene="SPBC2F12.15c"

/note="gtacgt, splice donor sequence"

1290..1307

/gene="SPBC2F12.15c"

/note="ctaacacttcgttccatg, splice branch and acceptor"

3582..3588

/gene="SPBC2F12.14c"

join(3582..4038..4371..5488)

/gene="SPBC2F12.14c"

/note="SPBC2F12.14c, len:52aa, similarity: to IMH2_YEAST P50095, probable inosine-5'-monophosphate dehydrogenase (52 .3aa), fasta scores, opt:2200, E():0, (62 .8% identity in 52 aa overlap)"

/codon_start=1

/label="SPBC2F12.14c"

/product="probable inosine-5'-monophosphate dehydrogenase"

/protein_id="CAB10161.1"

/db_xref="GI:2239243"

/translation="MSAAPPYTYEAELEVLLKKYKEKDGSLIDDLLRHNFGGLTFNDLFLI LPGYIDFVNNSVLETRIERNIVLKTPMSSPMDTVTDMATYMLAIGGIGVTHHNC TPEBGAAWRKVKVYENGFLDPVFSQPHDNTVTEVTPREBLITAEGISULRANEMLRSKKGKLPVVD KDDNIVALLSLLTDLMKNNHPLAKSTSSTDKOLMAYAAAGTRDDRTRALLAEGLDA VVIDSQQNSCQFIMKVKYTPKIVDIAGNVTRGGTASLAAAGDGLRVGMGSG SACITQEVNACGRQFATLQAQVAFASOGVQYDGGTQVNGHMKVSLGATAVMM GGLAGATESPGEYVREGRQYSYRGNSIAAMEGTGYNKAStGRTFSENDAVRVA REGDQGFTAYEKLY"

join(3951..4038..4371..4429)

/gene="SPBC2F12.14c"

/note="Match to PF00571 CBS, CBS domain Score 26.72"

4039..4370

/gene="SPBC2F12.14c"

/note="confirmed intron"

4039..4044

/gene="SPBC2F12.14c"

/note="gtaaat, splice donor sequence"

4208..4288

/gene="SPBC2F12.14c"

/note="putative snoRNA Sp-snR54, complements: Sp-18S_rRNA and modifies Am989. Yeast snR54 homolog. (Todd Lowe)"

4360..4370

/gene="SPBC2F12.14c"

/note="Match to PF00571 CBS, CBS domain Score 26.72"

4463..4465..4621

/gene="SPBC2F12.14c"

/note="Match to PF00571 CBS, CBS domain Score 46.07"

4715..5380

/gene="SPBC2F12.14c"

/note="Match to PF00478 IMPDH C, IMP dehydrogenase / GMP reductase C terminus Score 363.99"

complement(5821..5828)

/gene="SPBC2F12.13"

/note="Match to PF00478 IMPDH C, IMP dehydrogenase / GMP reductase C terminus Score 363.99"

5821..5828

/codon_start=1

/label="SPBC2F12.13"

/product="kinase-like protein"

/protein_id="CAB10160.1"

/db_xref="GI:2239242"

/db_xref="SWISS-PROT:O14343"

/translation="MSROSITITVYRPLFESTAESANLJASSDRUSFGTSSSLRNPGGS GQRIIRWKVLDGRVLYLFDEDETALSATRNLSTOSLARLSRSNNSAFRGDL RYAFDRVPEDETAQQQYERTFAYATGCGKTTHTIS7MQD PGLYLTKEKFMDHURDEKEIDRLRSLEYNETIDLLYSPTPNPAKUNLRL ADDRITVPLGTSISLSPESLEELIDIMKGKGNANRPTMSPETEANAASSRSHAVLQVTLIQKP

RTAGINEDEITLATUSIIDIAGSERATATKLRGSRPILEGANTINKSLLALGNCINALCDP
 HRRAHYPYDTSKTRKLPSLGNCRTVAYCVPSPSYHEETHNLKYARAKNKT
 EVLRNMISVHDYHOSYVKARVELLEQIENRLAQIDUSQNGSDQDVAQFSAHE
 SKLAFAARNLRRMTFFETLPQDNTIKEVKVKEFDQDSRVLKWLSCYERULLPNSADE
 RVFLYRSKLSKUESSLTERRAONKVDBEFPTYLESLKASSKELKEGMQELFSILEKWLQE
 VDLKLSTIENQVOLDAONKVDBEFPTYLESLKASSKELKEGMQELFSILEKWLQE
 IGLGERPNPLKVSSESKLINTSDSRTINDRVSEFTPTOLLNNLPMFVSKPKP
 VVFSKRSPKRVRVDFDISMSTSDFSGASAYNSPIQSCKLMNNFNTMHPSTPAHKRP
 NKNQDVEINUTSPVSPMLDKPEPGLLKPLEKQEVNEESTOOLDQLLAEQSSTD
 VSLPHDDEITLDDGSPVPKVDPDNFGRANMSPFTILNEAHNFDSKFKTRQSSL
 TTLHLSPNATIRKSLSMANEEERAK"

misc_feature complement("7219_8163")
 /gene="SPBCF2F12_13"
 /note="Match to PF00225 kinesin, Kinesin motor domain
 Score 362.06"
 complement("8020_8043")
 complement("8020_8043")
 /gene="SPBCF2F12_13"
 /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
 complement("8442_8455")
 complement("8442_8455")

misc_feature Query Match 1.4%; Score 19; DB 8; Length 38012;
 Best Local Similarity 100%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Complete sequence.

misc_feature QY 1197 atcatccaaacatgaa 1215
 Db 8555 ATCATCCAAACAGATGAA 8573

RESULT 12
 AB016875/c LOCUS AB016875 60476 bp DNA PLN 20-NOV-1999
 DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9D7,
 complete sequence.
 ACCESSION AB016875.1
 VERSION G1:3449316
 KEYWORDS HTG.
 SOURCE Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui TAC
 clone:K9D7.
 Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta;
 Eukarya; Viridiplantae; Spermatophyta; Magnoliophyta; eudicotyledons; core
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 Arabidopsis.
 1 (sites)

REFERENCE Nakamura.Y.
 AUTHORS Structural Analysis of Arabidopsis thaliana Chromosome 5. VIII
 TITLE Unpublished (1998)
 JOURNAL 2 (bases 1 to 60476)

REFERENCE Nakamura.Y.
 AUTHORS Direct Submission (18-AUG-1998) to the DDBJ/EMBL/GenBank databases.
 TITLE Submitted (18-AUG-1998) to the DDBJ/EMBL/GenBank databases.
 JOURNAL Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of
 Gene Structure 2; 1532-3, Yata, Kisarazu, Chiba 292, Japan
 (E-mail: ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
 Fax:+81-438-52-3934)

FEATURES Source
 1. .60476 "Arabidopsis thaliana"
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /chromosome="5"
 /clone="K9D7"
 /clone_lib="Mitsui TAC"
 BASE COUNT 19833 a 9701 c 10325 g 20617 t
 ORIGIN

Query Match 1.4%; Score 19; DB 7; Length 60476;
 Best Local Similarity 100.0%; Pred. NO. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1037 tcctcagccgtacggcg 1055

Db 35339 TCTTCAGCCTCGACCGGG 35321

RESULT 13
 AC002415 LOCUS AC002415 93419 bp DNA HTG 12-AUG-1997
 DEFINITION Homo sapiens chromosome X clone bWXD142, *** SEQUENCING IN PROGRESS
 *** , 6 unordered pieces.

ACCESSION AC002415
 VERSION AC002415.1 GI:2323256
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 93419)
 AUTHORS Chei, E.; Brownstein, B.H.; States, D.J.; Schlessinger, D. and Mazzaressa, R.

TITLE Direct Submission (12-AUG-1997)
 JOURNAL Washington University School of Medicine, 4566 Scott Avenue, St. Louis, MO 63110, USA
 COMMENT Current status of this project is available at:
http://genome.wustl.edu/cgm/seq_projects.html
 Submitted by:

and

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 Applied Biosystems Division of Perkin Elmer Corp.,
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and

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 St. Louis, MO 63108 USA
 e-mail: states@ibc.wustl.edu

* Note: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 9560: contig of 9560 bp in length
 * 25127: contig of 15567 bp in length
 * 45675: contig of 20548 bp in length
 * 73399: contig of 27724 bp in length
 * 45676: 82075: contig of 8676 bp in length
 * 73400: 82076: 93419: contig of 11344 bp in length.

FEATURES Source
 1. .93419
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="bWXD142"

BASE COUNT 25991 a /chromosome="X" 20209 c 20209 g 26030 t
 ORIGIN

Query Match 1.4%; Score 19; DB 32; Length 93419;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ORIGIN

Qy 810 attcatggcatactcccttt 828
 Db 4421 ATTCAATGGCATACTCCCTTT 4439

RESULT 14
 MOSTHREX17 247 bp DNA ROD
 Locus MUSTHREX17 247 bp DNA ROD
 DEFINITION Mouse thrombospondin (THBS1) gene, exon 17.
 ACCESSION M62465 S79284
 KEYWORDS M62465 .1 GI:202015
 SEGMENT Glycoprotein; thrombospondin.
 SOURCE Mus musculus (strain BALB/c, sub_species domesticus) DNA.
 ORGANISM Eukaryota; Metazoa; Chordata; Scleroglathri; Muridae; Murinae; Mus.
 REFERENCE Lawler,J., Duquette,M., Ferro,P., Copeland,N.G., Gilbert,D.J. and Jenkins,N.A.
 AUTHORS
 TITLE Characterization of the murine thrombospondin gene
 JOURNAL Genomics 11 (3), 58-600 (1993).
 MEDLINE 92128941
 FEATURES Location/qualifiers
 source 1..247
 /organism="Mus musculus"
 /strain="BALB/C"
 /sub_species="domesticus"
 /db_xref="taxon:10090"
 intron <1..6
 /gene="THBS1"
 /number=16
 exon 7..241
 /gene="THBS1"
 /number=17
 /db_xref="taxon:10090"
 intron >247
 /gene="THBS1"
 /number=17
 BASE COUNT 73 a 64 c 64 g 46 t
 ORIGIN

Query Match 1.3%; Score 18; DB 12; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ORIGIN

Qy 817 ggcatctccatggccatc 834
 Db 153 GGCACTCTCTTGCATC 136

RESULT 15
 G14673/c Locus G14673 400 bp DNA
 DEFINITION human STR SHGC-11830.
 ACCESSION G14673
 VERSION G14673.1 GI:1130412
 KEYWORDS STR sequence; primer; sequence tagged site.
 SOURCE Human.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
 Cetartiodactyla; Hominidae; Homo.

REFERENCE 1 (bases 1 to 400)
 AUTHORS Myers, R.M.
 JOURNAL Unpublished (1995)
 COMMENT Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 415/7259687
 Fax: 415/7259689
 Email: myers@shgc.stanford.edu

Primer A: CTAGGAAACCATTTGTCAGCC
 Primer B: GTCTCATTTGTTACGCCATCC
 STS size: 131
 PCR Profile:
 Initial incubation: 94 degrees C for 90 seconds
 Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600

Protocol:
 Template: 25 ng
 Primer: each 1 uM
 DNTPS: each 200 uM
 Taq Polymerase: 0.05 units/uL
 Total Vol: 10 uL

Buffer: MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3

FEATURES Location/Qualifiers
 source 1..400
 /organism="Homo sapiens"
 STS 121..251
 primer_bind 121..142
 primer_bind complement(229..251)
 BASE COUNT 113 a 85 c 88 g 114 t
 ORIGIN

Prepared with primer pairs derived from T62818 - Merck/Unibest.

Query Match 1.3%; Score 18; DB 13; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 cattacccttcagacaca 1283
 Db 357 CATTACCCCTCACAGACACA 340

Search completed: April 14, 2000, 18:33:06
 Job time: 8214 sec

c 253	14	1.0	159	1	T40843	Serine protease of Human gene signatu	326	14	1.0	V89105	
	166	1	166	1	T222272	Mutated human immu	328	14	1.0	N9026	
	255	14	1.0	177	1	T43883	Mutated human immu	c 329	14	1.0	N92096
	256	14	1.0	177	1	T27788	Mutated human immu	330	14	1.0	X40927
c 257	14	1.0	195	1	T67548	H. pylori secreted	331	14	1.0	V70394	
c 258	14	1.0	198	1	V24785	H. pylori ORF 06ep	332	14	1.0	Q68187	
c 259	14	1.0	200	1	X39511	Human secreted pro	333	14	1.0	Q84033	
c 260	14	1.0	215	1	V76480	Staphylococcus aur	333	14	1.0	Q95148	
c 261	14	1.0	219	1	Q43595	Synthetic PTHIP ge	334	14	1.0	V86576	
	262	14	1.0	240	1	Q11971	AARR scorpion toxi	c 335	14	1.0	Q68188
	263	14	1.0	252	1	T67640	H. pylori secreted	c 336	14	1.0	Q84005
c 264	14	1.0	259	1	T23925	Human gene signatu	c 337	14	1.0	EST clone D1516.	
c 265	14	1.0	265	1	Q04648	Modified kringle d	c 338	14	1.0	N	
c 266	14	1.0	271	1	V76480	Staphylococcus aur	c 339	14	1.0	Primer binding to	
c 267	14	1.0	274	1	T25165	Human gene signatu	340	14	1.0	DNA sequence of mo	
	268	14	1.0	297	1	T26581	Human gene signatu	341	14	1.0	Mouse cryptdin 5 g
c 269	14	1.0	303	1	V89591	EST clone CN951.	342	14	1.0	Hypersensitive res	
c 270	14	1.0	315	1	Q84029	N	c 343	14	1.0	EST clone Aw106.	
c 271	14	1.0	317	1	V90674	PMON5974 encodes (c 344	14	1.0	N	
c 272	14	1.0	321	1	Q59801	Nucleotide sequenc	345	14	1.0	Primer binding to	
c 273	14	1.0	321	1	V90720	Human brain Express	346	14	1.0	DNA sequence of mo	
c 274	14	1.0	323	1	T27924	Nucleotide sequenc	c 347	14	1.0	Delta2 (cell line	
c 275	14	1.0	323	1	T27167	PRLLS gene exon 2	c 348	14	1.0	Mycobacterium vac	
c 276	14	1.0	330	1	Q84025	PRLLS coding seque	c 349	14	1.0	M. vaccae antigen	
c 277	14	1.0	331	1	V87021	PMON5968 encodes (350	14	1.0	H. pylori secreted	
c 278	14	1.0	332	1	Q68095	EST clone BG142.	351	14	1.0	Clone C-11-3 from	
c 279	14	1.0	333	1	Q68092	N	352	14	1.0	Rice Glycogenin c1	
c 280	14	1.0	333	1	Q68102	Sequence encoding	c 353	14	1.0	Primer binding to	
c 281	14	1.0	333	1	Q68096	Sequence encoding	c 354	14	1.0	Polynucleotide seq	
c 282	14	1.0	333	1	Q68104	Sequence encoding	c 355	14	1.0	Primer binding to	
c 283	14	1.0	333	1	Q68097	Sequence encoding	c 356	14	1.0	Delta3 (cell line	
c 284	14	1.0	333	1	Q68103	Sequence encoding	c 357	14	1.0	Delta2 (cell line	
c 285	14	1.0	333	1	Q68093	Sequence encoding	c 358	14	1.0	Yeast presequence	
c 286	14	1.0	333	1	Q68098	Sequence encoding	c 359	14	1.0	Human secreted pro	
c 287	14	1.0	333	1	Q68099	Sequence encoding	c 360	14	1.0	Enterococcus faeca	
c 288	14	1.0	336	1	Q84007	PMON5901 encodes (c 361	14	1.0	Guanylate cyclase	
c 289	14	1.0	336	1	Q84009	PMON5901 encodes (c 362	14	1.0	Human GCAP-II prec	
c 290	14	1.0	336	1	Q84010	PMON5969 encodes (c 363	14	1.0	Cryptosporidium pa	
c 291	14	1.0	336	1	Q84011	PMON5916 encodes (c 364	14	1.0	Sequence of adult	
c 292	14	1.0	336	1	Q84012	PMON5941 encodes (c 365	14	1.0	Sequence of yeast	
c 293	14	1.0	336	1	Q84013	PMON5976 encodes (c 366	14	1.0	Sequence of prion	
c 294	14	1.0	336	1	Q84014	PMON5941 encodes (c 367	14	1.0	H. pylori secreted	
c 295	14	1.0	336	1	Q84015	PMON5960 encodes (c 368	14	1.0	Sequence of adult	
c 296	14	1.0	336	1	Q84022	PMON5961 encodes (c 369	14	1.0	Sequence of yeast	
c 297	14	1.0	336	1	Q84023	PMON5962 encodes (c 370	14	1.0	Sequence of yeast	
c 298	14	1.0	336	1	Q84024	PMON5963 encodes (c 371	14	1.0	Sequence of yeast	
c 299	14	1.0	336	1	Q84026	PMON5970 encodes (c 372	14	1.0	Sequence of yeast	
c 300	14	1.0	336	1	Q84027	PMON5970 encodes (c 373	14	1.0	Sequence of yeast	
c 301	14	1.0	336	1	Q84028	PMON5973 encodes (c 374	14	1.0	Sequence of yeast	
c 302	14	1.0	336	1	Q84030	PMON5975 encodes (c 375	14	1.0	Sequence of yeast	
c 303	14	1.0	336	1	Q84031	PMON5977 encodes (c 376	14	1.0	Sequence of yeast	
c 304	14	1.0	336	1	Q84032	PMON5982 encodes (c 377	14	1.0	Sequence of yeast	
c 305	14	1.0	336	1	Q84033	PMON5983 encodes (c 378	14	1.0	Sequence of yeast	
c 306	14	1.0	336	1	Q84034	PMON5983 encodes (c 379	14	1.0	Sequence of yeast	
c 307	14	1.0	336	1	Q84035	PMON5987 encodes (c 380	14	1.0	Sequence of yeast	
c 308	14	1.0	336	1	Q84036	PMON5987 encodes (c 381	14	1.0	Sequence of yeast	
c 309	14	1.0	336	1	Q84037	PMON5987 encodes (c 382	14	1.0	Sequence of yeast	
c 310	14	1.0	336	1	Q84038	PMON5987 encodes (c 383	14	1.0	Sequence of yeast	
c 311	14	1.0	336	1	Q84039	PMON5987 encodes (c 384	14	1.0	Sequence of yeast	
c 312	14	1.0	336	1	Q84040	PMON5987 encodes (c 385	14	1.0	Sequence of yeast	
c 313	14	1.0	336	1	Q84041	PMON5987 encodes (c 386	14	1.0	Sequence of yeast	
c 314	14	1.0	336	1	Q84042	PMON5987 encodes (c 387	14	1.0	Sequence of yeast	
c 315	14	1.0	336	1	Q84043	PMON5987 encodes (c 388	14	1.0	Sequence of yeast	
c 316	14	1.0	336	1	Q84044	PMON5987 encodes (c 389	14	1.0	Sequence of yeast	
c 317	14	1.0	336	1	Q84045	PMON5987 encodes (c 390	14	1.0	Sequence of yeast	
c 318	14	1.0	336	1	Q84046	PMON5987 encodes (c 391	14	1.0	Sequence of yeast	
c 319	14	1.0	336	1	Q84047	PMON5987 encodes (c 392	14	1.0	Sequence of yeast	
c 320	14	1.0	336	1	Q84048	PMON5987 encodes (c 393	14	1.0	Sequence of yeast	
c 321	14	1.0	336	1	Q84049	PMON5987 encodes (c 394	14	1.0	Sequence of yeast	
c 322	14	1.0	336	1	Q84050	PMON5987 encodes (c 395	14	1.0	Sequence of yeast	
c 323	14	1.0	336	1	Q84051	PMON5987 encodes (c 396	14	1.0	Sequence of yeast	
c 324	14	1.0	336	1	Q84052	PMON5987 encodes (c 397	14	1.0	Sequence of yeast	
c 325	14	1.0	336	1	Q84053	PMON5987 encodes (c 398	14	1.0	Sequence of yeast	

c 399	1.0	807	1	098735	Human GDF-1(fx) mo
c 400	1.0	828	1	T68075	Human GDF-1(fx) mo
c 401	1.0	839	1	V34717	cDNA sequence encc
c 402	1.0	840	1	X20014	Human GDF-1 cDNA,
c 403	1.0	845	1	T66947	Human GDF-1 (fx) P
c 404	1.0	850	1	T40855	Human GDF-1 cDNA.
c 405	1.0	857	1	V75197	Insert from PIGL e
c 406	1.0	858	1	V45175	Human body weight
c 407	1.0	861	1	V43021	Human C5 gene cDNA
c 408	1.0	867	1	T74471	S erythraea erythr
c 409	1.0	879	1	T01341	Encodes exon I of
c 410	1.0	894	1	N70391	Phaffia rhodozyma
c 411	1.0	894	1	N70036	cDNA encoding orn1
c 412	1.0	897	1	V24697	Human T-cell leuke
c 413	1.0	912	1	V46315	Helicobacter pylop
c 414	1.0	913	1	Q70048	Brassica thioester
c 415	1.0	925	1	T15611	Brassica campestr
c 416	1.0	925	1	V16740	Brassica acyl thiol
c 417	1.0	940	1	X21054	K. pneumoniae alco
c 418	1.0	945	1	V90853	Canine cholecystok
c 419	1.0	945	1	X25733	Human ZP3 gene. Hu
c 420	1.0	950	1	Q11972	Barley Ltp2 gene.
c 421	1.0	954	1	X20092	Green fluorescent
c 422	1.0	954	1	V55148	Mouse haemocytob
c 423	1.0	963	1	V55150	Bovine rotavirus V
c 424	1.0	963	1	X37469	Rabies virus nucle
c 425	1.0	971	1	X37479	Kurthia sp. biotin
c 426	1.0	972	1	V55149	Human secreted pro
c 427	1.0	972	1	V55151	Canine cholecystok
c 428	1.0	981	1	V12756	DNA encoding a S-
c 429	1.0	981	1	X16591	Onchoecoccus volvul
c 430	1.0	1001	1	X20478	H. pylori outer me
c 431	1.0	1004	1	X13479	DNA encoding an an
c 432	1.0	1017	1	V24931	H. pylori GHP0 525
c 433	1.0	1023	1	X13585	Sequence encoding
c 434	1.0	1023	1	X34232	Cytochrome C gene.
c 435	1.0	1025	1	V18441	Enterococcus faeca
c 436	1.0	1034	1	X14407	Mycobacterium tube
c 437	1.0	1068	1	X13571	M. tuberculosis
c 438	1.0	1083	1	T14024	Sequence 58
c 439	1.0	1095	1	V99747	Sequence encoding
c 440	1.0	1097	1	V44860	Staphylococcus aur
c 441	1.0	1101	1	V25033	DNA encoding a sul-
c 442	1.0	1101	1	V25034	Enterococcus faeca
c 443	1.0	1103	1	V05139	Enterococcus faeca
c 444	1.0	1110	1	V24662	Drosophila dCREB2-
c 445	1.0	1115	1	V48115	IL-1 alpha proprie
c 446	1.0	1116	1	V25108	Clone BG142-1 codi
c 447	1.0	1125	1	N91423	H. pylori cell env
c 448	1.0	1125	1	Q70705	Unknown DNA sequen
c 449	1.0	1125	1	T67935	H. pylori cell env
c 450	1.0	1127	1	V12757	Enteroecoccus faecalis
c 451	1.0	1138	1	X14134	H. pylori ORF 05gp
c 452	1.0	1140	1	V71081	Nucleotide sequenc
c 453	1.0	1143	1	T34428	H. pylori ORF 06ap
c 454	1.0	1187	1	V74711	Sequence of heat-r
c 455	1.0	1200	1	Q05728	Plasmin receptor D
c 456	1.0	1200	1	V24559	H. pylori cytoplasm
c 457	1.0	1200	1	V74138	Full length mouse
c 458	1.0	1204	1	X14194	Mouse FLAME-2 cDNA
c 459	1.0	1204	1	X14013	H. pylori GHP0 885
c 460	1.0	1221	1	X30447	Nicotinamide aden
c 461	1.0	1224	1	T15958	H. pylori secreted
c 462	1.0	1224	1	T67867	Staphylococcus aur
c 463	1.0	1224	1	Q58033	Human GDF-1 coding
c 464	1.0	1236	1	Q70537	Morphogen GDF-1 co
c 465	1.0	1239	1	T68012	Human morphogenic
c 466	1.0	1239	1	X07132	Human GDF-1(fx) mo
c 467	1.0	1239	1	X07112	Autographa califor
c 468	1.0	1247	1	Q41354	Human GDF-1 mo
c 469	1.0	1247	1	Q38862	Insert from clone
c 470	1.0	1247	1	Q58055	Drosophila inhibit
c 471	1.0	1247	1	Q67315	Protease from S. A

c 545	14	1.0	1576	1	Q10226	DNA encoding PGEM-hRARGam
					v84358	Streptococcus pneumoniae
					1	Protease from S. A
					1584	H. pylori inner membrane
					1	H. pylori cell env
					1586	H. pylori
					1	O27987
					X13606	Enterococcus faeca
					1	Human uncoupling P
					1587	Full length human
					1	Atrazine chlorhyd
					14658	DNA marker of meta
					1	DNA affinity nerve
					1592	Human adrenergic r
					1	Baculovirus ISP DN
					1605	AAVA Rep 68 gene.
					1	Human respiration
					1611	Vampire bat Plasmi
					1612	Sequence encoding
					1620	Helicobacter polyp
					1630	Cytochrome P450 ho
					1630	Alpha-1,3/4-fucosi
					1630	Macaque mucosal ad
					1631	M. tuberculosis RN
					1633	Atrazine chlorhyd
					1633	CDK2'-green fluores
					1634	Green fluorescent
					1635	Helicobacter polyp
					1635	Alpha-1,3/4-fucosi
					1636	Macaque mucosal ad
					1637	M. tuberculosis RN
					1638	Atrazine chlorhyd
					1639	CDK2'-green fluores
					1640	Green fluorescent
					1641	Helicobacter polyp
					1642	Alpha-1,3/4-fucosi
					1643	Macaque mucosal ad
					1644	M. tuberculosis RN
					1645	Atrazine chlorhyd
					1646	CDK2'-green fluores
					1647	Green fluorescent
					1648	Helicobacter polyp
					1649	Alpha-1,3/4-fucosi
					1650	Macaque mucosal ad
					1651	M. tuberculosis RN
					1652	Atrazine chlorhyd
					1653	CDK2'-green fluores
					1654	Green fluorescent
					1655	Helicobacter polyp
					1656	Alpha-1,3/4-fucosi
					1657	Macaque mucosal ad
					1658	M. tuberculosis RN
					1659	Atrazine chlorhyd
					1660	CDK2'-green fluores
					1661	Green fluorescent
					1662	Helicobacter polyp
					1663	Alpha-1,3/4-fucosi
					1664	Macaque mucosal ad
					1665	M. tuberculosis RN
					1666	Atrazine chlorhyd
					1667	CDK2'-green fluores
					1668	Green fluorescent
					1669	Helicobacter polyp
					1670	Alpha-1,3/4-fucosi
					1671	Macaque mucosal ad
					1672	M. tuberculosis RN
					1673	Atrazine chlorhyd
					1674	CDK2'-green fluores
					1675	Green fluorescent
					1676	Helicobacter polyp
					1677	Alpha-1,3/4-fucosi
					1678	Macaque mucosal ad
					1679	M. tuberculosis RN
					1680	Atrazine chlorhyd
					1681	CDK2'-green fluores
					1682	Green fluorescent
					1683	Helicobacter polyp
					1684	Alpha-1,3/4-fucosi
					1685	Macaque mucosal ad
					1686	M. tuberculosis RN
					1687	Atrazine chlorhyd
					1688	CDK2'-green fluores
					1689	Green fluorescent
					1690	Helicobacter polyp
					1691	Alpha-1,3/4-fucosi
					1692	Macaque mucosal ad
					1693	M. tuberculosis RN
					1694	Atrazine chlorhyd
					1695	CDK2'-green fluores
					1696	Green fluorescent
					1697	Helicobacter polyp
					1698	Alpha-1,3/4-fucosi
					1699	Macaque mucosal ad
					1700	M. tuberculosis RN
					1701	Atrazine chlorhyd
					1702	CDK2'-green fluores
					1703	Green fluorescent
					1704	Helicobacter polyp
					1705	Alpha-1,3/4-fucosi
					1706	Macaque mucosal ad
					1707	M. tuberculosis RN
					1708	Atrazine chlorhyd
					1709	CDK2'-green fluores
					1710	Green fluorescent
					1711	Helicobacter polyp
					1712	Alpha-1,3/4-fucosi
					1713	Macaque mucosal ad
					1714	M. tuberculosis RN
					1715	Atrazine chlorhyd
					1716	CDK2'-green fluores
					1717	Green fluorescent
					1718	Helicobacter polyp
					1719	Alpha-1,3/4-fucosi
					1720	Macaque mucosal ad
					1721	M. tuberculosis RN
					1722	Atrazine chlorhyd
					1723	CDK2'-green fluores
					1724	Green fluorescent
					1725	Helicobacter polyp
					1726	Alpha-1,3/4-fucosi
					1727	Macaque mucosal ad
					1728	M. tuberculosis RN
					1729	Atrazine chlorhyd
					1730	CDK2'-green fluores
					1731	Green fluorescent
					1732	Helicobacter polyp
					1733	Alpha-1,3/4-fucosi
					1734	Macaque mucosal ad
					1735	M. tuberculosis RN
					1736	Atrazine chlorhyd
					1737	CDK2'-green fluores
					1738	Green fluorescent
					1739	Helicobacter polyp
					1740	Alpha-1,3/4-fucosi
					1741	Macaque mucosal ad
					1742	M. tuberculosis RN
					1743	Atrazine chlorhyd
					1744	CDK2'-green fluores
					1745	Green fluorescent
					1746	Helicobacter polyp
					1747	Alpha-1,3/4-fucosi
					1748	Macaque mucosal ad
					1749	M. tuberculosis RN
					1750	Atrazine chlorhyd
					1751	CDK2'-green fluores
					1752	Green fluorescent
					1753	Helicobacter polyp
					1754	Alpha-1,3/4-fucosi
					1755	Macaque mucosal ad
					1756	M. tuberculosis RN
					1757	Atrazine chlorhyd
					1758	CDK2'-green fluores
					1759	Green fluorescent
					1760	Helicobacter polyp
					1761	Alpha-1,3/4-fucosi
					1762	Macaque mucosal ad
					1763	M. tuberculosis RN
					1764	Atrazine chlorhyd
					1765	CDK2'-green fluores
					1766	Green fluorescent
					1767	Helicobacter polyp
					1768	Alpha-1,3/4-fucosi
					1769	Macaque mucosal ad
					1770	M. tuberculosis RN
					1771	Atrazine chlorhyd
					1772	CDK2'-green fluores
					1773	Green fluorescent
					1774	Helicobacter polyp
					1775	Alpha-1,3/4-fucosi
					1776	Macaque mucosal ad
					1777	M. tuberculosis RN
					1778	Atrazine chlorhyd
					1779	CDK2'-green fluores
					1780	Green fluorescent
					1781	Helicobacter polyp
					1782	Alpha-1,3/4-fucosi
					1783	Macaque mucosal ad
					1784	M. tuberculosis RN
					1785	Atrazine chlorhyd
					1786	CDK2'-green fluores
					1787	Green fluorescent
					1788	Helicobacter polyp
					1789	Alpha-1,3/4-fucosi
					1790	Macaque mucosal ad
					1791	M. tuberculosis RN
					1792	Atrazine chlorhyd
					1793	CDK2'-green fluores
					1794	Green fluorescent
					1795	Helicobacter polyp
					1796	Alpha-1,3/4-fucosi
					1797	Macaque mucosal ad
					1798	M. tuberculosis RN
					1799	Atrazine chlorhyd
					1800	CDK2'-green fluores
					1801	Green fluorescent
					1802	Helicobacter polyp
					1803	Alpha-1,3/4-fucosi
					1804	Macaque mucosal ad
					1805	M. tuberculosis RN
					1806	Atrazine chlorhyd
					1807	CDK2'-green fluores
					1808	Green fluorescent
					1809	Helicobacter polyp
					1810	Alpha-1,3/4-fucosi
					1811	Macaque mucosal ad
					1812	M. tuberculosis RN
					1813	Atrazine chlorhyd
					1814	CDK2'-green fluores
					1815	Green fluorescent
					1816	Helicobacter polyp
					1817	Alpha-1,3/4-fucosi
					1818	Macaque mucosal ad
					1819	M. tuberculosis RN
					1820	Atrazine chlorhyd
					1821	CDK2'-green fluores
					1822	Green fluorescent
					1823	Helicobacter polyp
					1824	Alpha-1,3/4-fucosi
					1825	Macaque mucosal ad
					1826	M. tuberculosis RN
					1827	Atrazine chlorhyd
					1828	CDK2'-green fluores
					1829	Green fluorescent
					1830	Helicobacter polyp
					1831	Alpha-1,3/4-fucosi
					1832	Macaque mucosal ad
					1833	M. tuberculosis RN
					1834	Atrazine chlorhyd
					1835	CDK2'-green fluores
					1836	Green fluorescent
					1837	Helicobacter polyp
					1838	Alpha-1,3/4-fucosi
					1839	Macaque mucosal ad
					1840	M. tuberculosis RN
					1841	Atrazine chlorhyd
					1842	CDK2'-green fluores
					1843	Green fluorescent
					1844	Helicobacter polyp
					1845	Alpha-1,3/4-fucosi
					1846	Macaque mucosal ad
					1847	M. tuberculosis RN
					1848	Atrazine chlorhyd
					1849	CDK2'-green fluores
					1850	Green fluorescent
					1851	Helicobacter polyp
					1852	Alpha-1,3/4-fucosi
					1853	Macaque mucosal ad
					1854	M. tuberculosis RN
					1855	Atrazine chlorhyd
					1856	CDK2'-green fluores
					1857	Green fluorescent
					1858	Helicobacter polyp
					1859	Alpha-1,3/4-fucosi
					1860	M

691	14	1.0	2085	1	Q81504	OPDE 45 kDa subunit	c	764	14	1.0	X20299
692	14	1.0	2089	1	T31378	Human alpha-1C3 ad	c	765	14	1.0	T4794
693	14	1.0	2093	1	Q70541	Heliothis ecdisone	c	766	14	1.0	V7493
694	14	1.0	2098	1	X02558	Staphylococcus aure	c	767	14	1.0	T9675
695	14	1.0	2127	1	V23246	MSV-1 clone LTRGA	c	768	14	1.0	V43169
696	14	1.0	2133	1	N91042	Clone LTRGAG12 DNA	c	769	14	1.0	T34184
697	14	1.0	2137	1	Q05675	Pentachlorophenol	c	770	14	1.0	Q20690
698	14	1.0	2157	1	V71039	hGDP-1 and hGDP-1	c	771	14	1.0	T71032
699	14	1.0	2160	1	V71027	GrK5-green fluores	c	772	14	1.0	Q4937
700	14	1.0	2165	1	T14054	PPB gene. Novel	c	773	14	1.0	V71024
c 701	14	1.0	2169	1	X23320	Gr5-green fluores	c	774	14	1.0	Green fluorescent
c 708	14	1.0	2172	1	Q56930	Sequence encoding	c	775	14	1.0	Sequence encoding
c 703	14	1.0	2175	1	Q29268	Cytomegalovirus To	c	776	14	1.0	Cytomegalovirus To
c 704	14	1.0	2181	1	V71037	v-PA-beta. New fib	c	777	14	1.0	Q20690
705	14	1.0	2184	1	V71086	ERK2-green fluores	c	778	14	1.0	T47534
706	14	1.0	2192	1	T77838	Green fluorescent	c	779	14	1.0	V71076
c 707	14	1.0	2196	1	Q74211	Fungal signal reco	c	780	14	1.0	T98772
c 708	14	1.0	2196	1	T01112	CMVintA Promoter a	c	781	14	1.0	T9043
c 709	14	1.0	2199	1	T80052	Bacillus thuringie	c	782	14	1.0	V71075
710	14	1.0	2206	1	Q70754	Human calcium chan	c	783	14	1.0	N70917
c 711	14	1.0	2214	1	Q70731	PKB-green fluores	c	784	14	1.0	T47532
712	14	1.0	2217	1	Q66982	Protein tyrosine P	c	785	14	1.0	V71072
713	14	1.0	2220	1	T16542	Human melanoma ass	c	786	14	1.0	zap-0-green fluore
c 714	14	1.0	2220	1	T11022	CMVintA-GBH termin	c	787	14	1.0	DNA encoding trans
715	14	1.0	2247	1	V24920	Rice actin 1 gene	c	788	14	1.0	Sequene encoding
716	14	1.0	2247	1	V25134	Beta tubulin gene	c	789	14	1.0	Green fluorescent
c 717	14	1.0	2251	1	N30050	TRP-binding prote	c	790	14	1.0	Human
c 718	14	1.0	2251	1	X40195	Human betaine-GABA	c	791	14	1.0	partial rice pyruv
719	14	1.0	2255	1	T11240	Human betaine/GABA	c	792	14	1.0	Lactococcus lactis
720	14	1.0	2257	1	Q05674	Urochloa panicoidae	c	793	14	1.0	2,2-diakylglycine
c 721	14	1.0	2258	1	N60078	H. pylori ORF 05ae	c	794	14	1.0	Dialkylglycine dec
c 722	14	1.0	2262	1	X23322	H. pylori inner me	c	795	14	1.0	Solanum tuberosum
c 723	14	1.0	2265	1	T14530	Sequence encoding	c	796	14	1.0	Moraxella bovis mb
724	14	1.0	2270	1	N91184	Sequence encoding	c	797	14	1.0	Helicobacter leucon
c 725	14	1.0	2274	1	V90770	Human albumin gene	c	798	14	1.0	Partial rice pyruv
c 726	14	1.0	2280	1	N60395	Neisseria meningit	c	799	14	1.0	Human cytomegalovi
c 727	14	1.0	2290	1	Q89780	v-PA-alpha2. New f	c	800	14	1.0	Sequence encoding
c 728	14	1.0	2292	1	V84357	Recombinant human	c	801	14	1.0	HSV-2 strain SB5 C
729	14	1.0	2297	1	V58945	N. meningitidis st	c	802	14	1.0	Human brain Na+ de
c 730	14	1.0	2306	1	T31377	HS4-RC gamma RII g	c	803	14	1.0	Human sodium-1-lithi
c 731	14	1.0	2315	1	V07281	SpkB gene encoding	c	804	14	1.0	Human cytomegalovi
c 732	14	1.0	2330	1	Q20759	Nucleotide sequenc	c	805	14	1.0	Human cytomegalovi
733	14	1.0	2337	1	T94212	Sequence constitut	c	806	14	1.0	Murine guanine nuc
c 734	14	1.0	2338	1	Q13575	Human alpha 1C2 ad	c	807	14	1.0	Virulence determin
735	14	1.0	2341	1	V62155	Streptococcus pneu	c	808	14	1.0	Heliothis ecdisone
736	14	1.0	2343	1	V56302	Human alpha-1C2 ad	c	809	14	1.0	Mycobacterium bovi
c 737	14	1.0	2360	1	Q02888	Human semaphorin W	c	810	14	1.0	Rabbit protein-cou
c 738	14	1.0	2360	1	Q24438	Alkaline protease	c	811	14	1.0	B. thuringiensis to
739	14	1.0	2364	1	Q12632	Thermotoga maritim	c	812	14	1.0	Photohabdus lumen
c 740	14	1.0	2373	1	T45675	CD4-specific CDR-g	c	813	14	1.0	PKB-green fluores
c 741	14	1.0	2379	1	Q10548	Sequence encoding	c	814	14	1.0	polyhydroxybutyrate
c 742	14	1.0	2382	1	Q45987	Preproto-HSA-V1V2 fu	c	815	14	1.0	S receptor kinase
c 743	14	1.0	2384	1	Q46543	Preproto-HSA-G-CSF c	c	816	14	1.0	AS-30D tumour Type
c 744	14	1.0	2384	1	V09864	Drosophila SSRP co	c	817	14	1.0	H. pylori cell env
c 745	14	1.0	2387	1	V09624	D. melanogaster SS	c	818	14	1.0	p8Alpha-green floo
c 746	14	1.0	2387	1	Q48438	Brh-1 CDNA. Polype	c	819	14	1.0	Schwannomin-blindin
c 747	14	1.0	2394	1	V71088	Wasp Brh-1 toxin g	c	820	14	1.0	Hexokinase-glucoki
c 748	14	1.0	2394	1	V71087	NFKappaB p65 subu	c	821	14	1.0	Hexokinase-glucoki
c 749	14	1.0	2395	1	V08854	PKB-green fluores	c	822	14	1.0	Construct comprisi
c 750	14	1.0	2397	1	V71040	Nucleotide sequenc	c	823	14	1.0	Fungal signal rece
c 751	14	1.0	2418	1	T15598	Smad3-green fluores	c	824	14	1.0	p8Alpha-green floo
c 752	14	1.0	2421	1	V71028	Laccase-LCC1 gene.	c	825	14	1.0	Hexokinase-glucoki
c 753	14	1.0	2427	1	V07915	Green fluores	c	826	14	1.0	Construct comprisi
c 754	14	1.0	2430	1	Q04305	Helicobacter pylor	c	827	14	1.0	Apoptosis particip
c 755	14	1.0	2430	1	T61550	Coding region Of m	c	828	14	1.0	Human Tm2/B19 cdna
c 756	14	1.0	2430	1	V17655	Mouse interleukin	c	829	14	1.0	c
c 757	14	1.0	2430	1	V38332	Mouse interleukin-	c	830	14	1.0	V71026
c 758	14	1.0	2430	1	V08858	Mouse interleukin-	c	831	14	1.0	V00133
c 759	14	1.0	2430	1	X22407	Murine IL-4 recept	c	832	14	1.0	V2911
c 760	14	1.0	2433	1	T29395	Apoptosis particip	c	833	14	1.0	V00124
c 761	14	1.0	2434	1	T32864	Mus musculus SOCS1	c	834	14	1.0	V0098
c 762	14	1.0	2434	1	T32864	Tomato P119 gene P	c	835	14	1.0	V71035
c 763	14	1.0	2455	1	Q45988	G-CSF-(Gly)4-HSA C	c	836	14	1.0	Q86558

c	837	14	1.0	V20404	1	Plasmid R-H-R/SK # Construct comprising targetting region	
c	838	14	1.0	2955	1	Q86755	Synthetic hepatitis B construct
c	839	14	1.0	2962	1	X21498	Rat hexokinase I
c	840	14	1.0	2965	1	X39658	Rat hexokinase II
c	841	14	1.0	2971	1	N81166	Rat hexokinase III
c	842	14	1.0	2991	1	V71078	Rat hexokinase I
c	843	14	1.0	2991	1	X20288	Rat hexokinase I
c	844	14	1.0	2994	1	V29925	Phage resistance
c	845	14	1.0	2994	1	V71077	Staphylococcus aureus
c	846	14	1.0	3000	1	Q14319	Actin gene (incl.)
c	847	14	1.0	3000	1	Q14320	Actin. Novel polypeptide
c	848	14	1.0	3000	1	Q14320	Sf9 alpha-mannosidase
c	849	14	1.0	3000	1	Q26509	Bacillus thuringiensis
c	850	14	1.0	3012	1	V52012	A. chrysogenum act
c	851	14	1.0	3029	1	X20286	Sugar biosynthesis
c	852	14	1.0	3032	1	V20992	B. thuringiensis
c	853	14	1.0	3101	1	X14217	Actin gene
c	854	14	1.0	3105	1	T99905	New recombinant
c	855	14	1.0	3106	1	V02323	IkappaB kinase alpha
c	856	14	1.0	3107	1	V68092	Bacillus burgdorferi
c	857	14	1.0	3110	1	T84234	Gene fluorescent
c	858	14	1.0	3110	1	V53557	Pertactin antigen
c	859	14	1.0	3120	1	V71029	Pertactin antigen
c	860	14	1.0	3125	1	Q14320	Bordetella parapertactin
c	861	14	1.0	3131	1	Q73686	prn gene. DNA encodes
c	862	14	1.0	3131	1	Q66687	Helicobacter polypolymerase
c	863	14	1.0	3131	1	T99904	CNA encoding the
c	864	14	1.0	3131	1	V02322	Helicobacter polypolymerase
c	865	14	1.0	3131	1	V40561	Human thiazide-sensitive
c	866	14	1.0	3138	1	V71041	Green fluorescent protein
c	867	14	1.0	3141	1	T47556	HIV virus-1 (La)
c	868	14	1.0	3183	1	V09024	EHEC eae gene assosiation
c	869	14	1.0	3240	1	V48270	Enterohaemorrhagic
c	870	14	1.0	3245	1	V02322	Enterohaemorrhagic
c	871	14	1.0	3252	1	Q31650	Enteropathogenic
c	872	14	1.0	3303	1	Q14806	Bacillus thuringiensis
c	873	14	1.0	3311	1	T70377	Stat5: green fluorescent
c	874	14	1.0	3317	1	T97089	Staphylococcus faecalis
c	875	14	1.0	3339	1	V61096	Staphylococcus faecalis
c	876	14	1.0	3350	1	T08553	Staphylococcus faecalis
c	877	14	1.0	3358	1	V58005	Staphylococcus faecalis
c	878	14	1.0	3377	1	V64424	Staphylococcus faecalis
c	879	14	1.0	3412	1	X25772	Staphylococcus faecalis
c	880	14	1.0	3420	1	T75437	Mycobacterium tuberculosis
c	881	14	1.0	3423	1	X40183	Lung cancer association
c	882	14	1.0	3435	1	T079746	Mycobacterium tuberculosis
c	883	14	1.0	3445	1	Q48230	Acernonium chrysogaster
c	884	14	1.0	3445	1	Q55405	A. chrysogenum beta
c	885	14	1.0	3445	1	Q55406	S. erythraea erythromycin
c	886	14	1.0	3451	1	V02308	Cell membrane protein
c	887	14	1.0	3463	1	T85397	Pseudomonas fluorescens
c	888	14	1.0	3463	1	V16191	Alkaline cellulase
c	889	14	1.0	3471	1	V16516	DNA encoding a Bacillus optimised DNA
c	890	14	1.0	3474	1	Q39018	Insecticidal protein
c	891	14	1.0	3474	1	V00395	Sequence of pure maize optimised B.
c	892	14	1.0	3474	1	T74012	Human G1A cDNA. Design
c	893	14	1.0	3474	1	Q39020	Sequence of full 1
c	894	14	1.0	3474	1	T74013	Full length maize optimised DNA
c	895	14	1.0	3474	1	V16191	Maize optimised DNA
c	896	14	1.0	3478	1	V00291	Maize fluorescent protein
c	897	14	1.0	3484	1	V71083	NFAT1-green fluorescent
c	898	14	1.0	3505	1	Q35270	Expression vector
c	899	14	1.0	3508	1	T01115	VIR vaccination vector
c	900	14	1.0	3508	1	V16192	Expression vector
c	901	14	1.0	3516	1	V71083	Maize genomic clone
c	902	14	1.0	3546	1	V00395	42K promoted cytosolic
c	903	14	1.0	3547	1	T01115	Polylgalacturonase
c	904	14	1.0	3553	1	V21771	Human TATA-binding
c	905	14	1.0	3553	1	Q74208	Sequence encoding
c	906	14	1.0	3557	1	X04605	CMV 9B transmembrane
c	907	14	1.0	3567	1	T47559	CMV 9B transmembrane
c	908	14	1.0	3569	1	T85905	Human cyclin D1
c	909	14	1.0	3603	1	T42217	Human cyclin D1/CY

c	910	14	1.0	T79595	1	T79595	TATA-binding protein
c	911	14	1.0	3603	1	3610	Synthetic hepatitis B construct
c	912	14	1.0	3603	1	3615	Rat hexokinase I
c	913	14	1.0	3603	1	3635	Rat hexokinase II
c	914	14	1.0	3603	1	3647	Rat hexokinase I
c	915	14	1.0	3603	1	3647	Rat hexokinase I
c	916	14	1.0	3603	1	3704	Phage resistance
c	917	14	1.0	3603	1	3733	Staphylococcus aureus
c	918	14	1.0	3603	1	3748	Actin gene (incl.)
c	919	14	1.0	3603	1	3748	Actin. Novel polypeptide
c	920	14	1.0	3603	1	3748	Sf9 alpha-mannosidase
c	921	14	1.0	3603	1	3748	Bacillus thuringiensis
c	922	14	1.0	3603	1	3750	BT toxin
c	923	14	1.0	3603	1	3750	BT toxin 33F2. New
c	924	14	1.0	3603	1	3756	Bacillus thuringiensis Strain 33F2 DNA. D
c	925	14	1.0	3603	1	3771	33F2 toxin coding
c	926	14	1.0	3603	1	3771	Xenopus frog protein
c	927	14	1.0	3603	1	3771	Xenopus frog protein encoding a mer
c	928	14	1.0	3603	1	3771	Phospholipase C-gamma CDNA of leaderless
c	929	14	1.0	3603	1	3771	CDNA of leaderless phospholipase C-gamma
c	930	14	1.0	3603	1	3771	Streptococcus pneumoniae
c	931	14	1.0	3603	1	3771	Mouse pheromone receptor
c	932	14	1.0	3603	1	3796	Human tollloid-like cryt5 gene. Isola
c	933	14	1.0	3603	1	3796	CRYT5 gene. Isola
c	934	14	1.0	3603	1	3810	CDNA of leaderless
c	935	14	1.0	3603	1	3810	CDNA of leaderless
c	936	14	1.0	3603	1	3893	CDNA encoding Bacillus thuringiensis
c	937	14	1.0	3603	1	3895	CDNA encoding Bacillus thuringiensis
c	938	14	1.0	3603	1	3896	CDNA encoding Bacillus thuringiensis
c	939	14	1.0	3603	1	3919	CDNA encoding Bacillus thuringiensis
c	940	14	1.0	3603	1	3919	CDNA encoding Bacillus thuringiensis
c	941	14	1.0	3603	1	3934	CDNA encoding Bacillus thuringiensis
c	942	14	1.0	3603	1	3951	CDNA encoding Bacillus thuringiensis
c	943	14	1.0	3603	1	3951	CDNA encoding Bacillus thuringiensis
c	944	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	945	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	946	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	947	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	948	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	949	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	950	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	951	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	952	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	953	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	954	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	955	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	956	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	957	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	958	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	959	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	960	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	961	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	962	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	963	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	964	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	965	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	966	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	967	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	968	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	969	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	970	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	971	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	972	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	973	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	974	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	975	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	976	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	977	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	978	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	979	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	980	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	981	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	982	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	983	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	984	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	985	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	986	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	987	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	988	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	989	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	990	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	991	14	1.0	3603	1	3955	CDNA encoding Bacillus thuringiensis
c	992	14	1.0	3603	1	3955	CDNA encoding Bac

PT and produce antisense sequences to treat mycobacterial infections
 PS Disclosure: Fig 4A-I; 62pp; English.
 CC This is the DNA sequence of the Mycobacterium tuberculosis embCAB
 CC operon, which determines resistance to the antimycobacterial drug
 CC ethambutol (EMB). It includes the embA, embB and emb genes
 CC that encode proteins (see W7305-54) which are the target of
 CC action of M. tuberculosis for EMB. Wild-type and mutated embCAB
 CC nucleic acid sequences are useful e.g. as probes used in the
 CC diagnosis of drug-resistant mycobacteria or to determine the
 CC susceptibility of mycobacteria to EMB. The nucleic acids are also
 CC useful in the treatment of mycobacterial infections; anti-DNA or
 CC anti-tRNA sequences can be administered to inhibit embCAB operon
 CC mRNA activity (claimed). The invention additionally provides for
 CC the use of embCAB operon nucleic acid sequences as vaccines, or
 CC to improve existing vaccines. Sequence 10095 BP; 1469 A; 3475 C; 3370 G; 1780 T;

Query Match Score 18; DB 1; Length 10095;
 Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;

Qy 401 acggctacatctgttca 418
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1031 ACGGCTACATCTGTGACCA 1048

RESULT 4
 ID T19263 standard; cDNA to mRNA; 196 BP.
 AC T19263
 DT 28-JUN-1996 (first entry)
 DE Human gene signature HOMSG000280.
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.
 OS Homo sapiens.
 PN W09514772.A1.

PD 01-JUN-1995.
 PF 11-NOV-1994; J01916.
 PR 12-NOV-1993; JP-355504.

PA (OKUBI/) OKUBO K.
 PA Matsubara K, Okubo K;
 PI Matsubara K, Okubo K;
 DR WPI; 206931/27.

PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of correspond. mRNA in specific human
 PT tissues.

PS Claim 1: Page 345; 2245pp; Japanese.
 CC A single-stranded DNA (or its complementary strand or the correspond.
 CC double-stranded DNA) which comprises one of the 787 "GS" sequences
 CC given in T19001-T26837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared from
 CC various human tissues; synthesis of cDNA was initiated from the 3'-
 CC end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types. Sequence 196 BP; 59 A; 55 C; 34 G; 48 T;

Query Match Score 17; DB 1; Length 196;
 Best Local Similarity 100.0%; Pred. No. 35; Mismatches 0; Indels 0; Gaps 0;

SQ 709 accgacgttgcattcaa 725

Db 64 ACCGACGTGCGCATCAA 80

RESULT 5
 ID V31989 standard; DNA; 229 BP.
 AC V31989;
 DT 07-MAY-1998 (first entry)
 DE BS106 Polynucleotide clone 1662285 (1);
 KW ss; human; BS106; breast tissue gene; breast cancer; detection marker.
 OS Homo sapiens.
 PN W0981895-A1.
 PD 07-MAY-1998.
 PF 31-OCT-1997; US-742067.
 PA (ABBOT LAB.
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
 PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 DR WPI; 98-27234/24.
 PT Detecting BS106 gene products - useful for developing products for
 PT detecting, staging, preventing, treating or determining
 PT predisposition to e.g. breast cancer.
 PS Claim 1; Page 88; 114pp; English.
 CC BS106 is a breast tissue gene with which breast cancer and related
 CC diseases are associated. The BS106 polynucleotides V31989-V31993 can be
 CC detected by BS106 specific polynucleotides or complements acting as
 CC useful markers for detection methods. The products and methods can be
 CC used for detecting, diagnosing, staging, preventing or treating, or
 CC determining predisposition to diseases or conditions of the breast such
 CC as breast cancer.
 SQ Sequence 308 BP; 63 A; 94 C; 65 G; 86 T;

Query Match Score 17; DB 1; Length 229;
 Best Local Similarity 100.0%; Pred. No. 35; Mismatches 0; Indels 0; Gaps 0;

Qy 381 gggtttcatcatccaa 397
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 187 GGCGTCATCATCACCA 171

RESULT 6
 ID V31990 standard; DNA; 308 BP.
 AC V31990;
 DT 25-SEP-1998 (first entry)
 DE BS106 Polynucleotide clone 893988.
 KW ss; human; BS106; breast tissue gene; breast cancer; detection marker.
 OS Homo sapiens.
 PN W0981894-5-A1.
 PD 07-MAY-1998.
 PF 31-OCT-1997; U19836.
 PR 07-OCT-1996; US-742057.
 PA (ABBOT LAB.
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
 PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 DR WPI; 98-27234/24.
 PT Detecting BS106 gene products - useful for developing products for
 PT detecting, staging, preventing, treating or determining
 PT predisposition to e.g. breast cancer.
 PS Claim 1; Page 89; 114pp; English.
 CC BS106 is a breast tissue gene with which breast cancer and related
 CC diseases are associated. The BS106 polynucleotides V31989-V31993 can be
 CC detected by BS106 specific polynucleotides or complements acting as
 CC useful markers for detection methods. The products and methods can be
 CC used for detecting, diagnosing, staging, preventing or treating, or
 CC determining predisposition to diseases or conditions of the breast such
 CC as breast cancer.
 SQ Sequence 308 BP; 63 A; 94 C; 65 G; 86 T;

Query Match 1.2%; Score 17; DB 1; Length 308;
Best Local Similarity 100.0%; Pred. No. 35; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 381 99gcttcatcatcaga 397
Db 174 GGGCTTCATCATCAGCA 158

RESULT 7
V31992/c
ID V31992 standard; DNA; 482 BP.
AC V31992-
DT 25-SEP-1998 (first entry)
DE BS106: polynucleotide consensus sequence.
KW ss: human; BS106: breast tissue gene; breast cancer; detection marker.
OS Homo sapiens.
PN WO9818945-A1.
PD 07-MAY-1998.
PP 31-OCT-1997; U19836.
PR 31-OCT-1996; US-742067.
PA (ABBO) ABBOTT LAB.

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
PT Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
PI Roberts-Rapp L, Russell JC, Stroupe SD,
DR WPI; 98-27234/24.
PT detecting BS106 gene products - useful for developing products for
PT detecting, staging, preventing, treating or determining
PT predisposition to e.g. breast cancer
PS Claim 1; Page 88-114BP; English.
CC BS106 is a breast tissue gene with which breast cancer and related
CC diseases are associated. The BS106 polynucleotides V31989-V31993 can be
CC detected by BS106 specific polynucleotides or complements acting as
CC useful markers for detection methods. The products and methods can be
CC used for detecting, diagnosing, staging, preventing or treating, or
CC determining predisposition to diseases or conditions of the breast such
SQ Sequence 482 BP; 109 A; 136 C; 90 G; 145 T;

Query Match 1.2%; Score 17; DB 1; Length 482;
Best Local Similarity 100.0%; Pred. No. 36; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 381 99gcttcatcatcaga 397
Db 187 GGGCTTCATCATCAGCA 171

RESULT 8
X00704/c
ID X00704 standard; DNA; 489 BP.
AC X00704-
DT 25-MAR-1999 (first entry)
DE Human secreted protein gene 34 clone HMOAJ64.
KW Human; secreted protein fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN WO9812738-A1.
PD 01-OCT-1998.
PF 19-MAR-1998; U05311.
PR 30-MAY-1997; US-050937.
PR 21-MAR-1997; US-041277.
PR 21-MAR-1997; US-041281.

PR 21-MAR-1997; US-042344.
PR 30-MAY-1997; US-040069.
PR 30-MAY-1997; US-048094.
PR 30-MAY-1997; US-048095.
PR 30-MAY-1997; US-048096.
PR 30-MAY-1997; US-048099.
PR 30-MAY-1997; US-048131.
PR 30-MAY-1997; US-048135.
PR 30-MAY-1997; US-048154.
PR 30-MAY-1997; US-048160.
PR 30-MAY-1997; US-048186.
PR 30-MAY-1997; US-048187.
PR 30-MAY-1997; US-048188.
PR 30-MAY-1997; US-048197.
PR 30-MAY-1997; US-048251.
PR 30-MAY-1997; US-048355.
PR 05-AUG-1997; US-054804.

(HUNA-) HUMAN GENOME SCI INC.
PA Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS,
PI Rosen CA, Ruben SM, Shi Y, Young P;
DR WPI; 99-070666/06.
P-PSDB; W67900.

PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PT disorders, immune diseases, inflammation or blood disorders
PT (ABBOT) ABBOTT LAB.
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
PT Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
PI Roberts-Rapp L, Russell JC, Stroupe SD,
DR WPI; 98-27234/24.
PT detecting BS106 gene products - useful for developing products for
PT detecting, staging, preventing, treating or determining
PT predisposition to e.g. breast cancer
PS Claim 1; Page 88-114BP; English.
CC This sequence represents a nucleic acid molecule which encodes a secreted
CC human protein. The gene number, and the clone it is derived from, are
CC detailed in the descriptor line. The gene can be used to generate fusion
CC proteins by linking to the gene to a human immunoglobulin FC portion
CC (e.g. X00602) for increasing the stability of the fused protein as
CC compared to the human protein only.
CC The invention relates to 87 novel genes and their fragments (nucleic acid
CC sequences: X00611-X00724; amino acid sequences W67807-W68004), which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 87 polynucleotides, based on
CC which tissues they are most highly expressed in (see X00611 for described
CC uses).
SQ Sequence 489 BP; 124 A; 134 C; 91 G; 140 T;

Query Match 1.2%; Score 17; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 36; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 381 99gcttcatcatcaga 397
Db 181 GGCGTTCATCATCACGCA 165

RESULT 9
X00644/c
ID X00644 standard; DNA; 489 BP.
AC X00644-
DT 25-MAR-1999 (first entry)
DE Human secreted protein gene 34 clone HMOAJ64.
KW Human; secreted protein; fusion protein; gene therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN WO9812738-A1.
PD 01-OCT-1998.
PF 19-MAR-1998; U05311.
PR 30-MAY-1997; US-050937.
PR 21-MAR-1997; US-041277.
PR 21-MAR-1997; US-041281.
PR 19-MAR-1998; U05311.

PR 30-MAY-1997; US-050937.
 PR 21-MAR-1997; US-041276.
 PR 21-MAR-1997; US-041277.
 PR 21-MAR-1997; US-041281.
 PR 21-MAR-1997; US-042344.
 PR 30-MAY-1997; US-048069.
 PR 30-MAY-1997; US-048094.
 PR 30-MAY-1997; US-048095.
 PR 30-MAY-1997; US-048096.
 PR 30-MAY-1997; US-048099.
 PR 30-MAY-1997; US-048131.
 PR 30-MAY-1997; US-048135.
 PR 30-MAY-1997; US-048154.
 PR 30-MAY-1997; US-048160.
 PR 30-MAY-1997; US-048186.
 PR 30-MAY-1997; US-048187.
 PR 30-MAY-1997; US-048188.
 PR 30-MAY-1997; US-048330.
 PR 30-MAY-1997; US-048331.
 PR 30-MAY-1997; US-048352.
 PR 30-MAY-1997; US-048355.
 PR 05-AUG-1997; US-054355.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Brewer LA, Duan R, Ebner AM, Ferrie AM, Florence KA,
 Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS,
 PI Rosen CA, Ruben SM, Shi Y, Young P;
 DR WPI: 99-070066/06.
 DR P-PSDB; W67840.
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 disorders, immune diseases, inflammation or blood disorders
 PS Claim 1; Page 198; 385pp; English.
 CC This sequence represents a nucleic acid molecule which encodes a secreted
 human protein. The gene number, and the clone it is derived from, are
 detailed in the descriptor line. The gene can be used to generate fusion
 proteins by linking to the gene to a human immunoglobulin Fc portion
 (e.g. X00602) for increasing the stability of the fused protein as
 compared to the human protein only.
 CC The invention relates to 87 novel genes and their fragments (nucleic acid
 sequences: X00611-X00724; amino acid sequences W67807-W68004) which
 CC are useful for preventing, treating or ameliorating medical conditions
 e.g. by protein or gene therapy. Also, pathological conditions can be
 diagnosed by determining the amount of the new polypeptides in a sample
 or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 87 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X00611 for described
 CC uses).
 Sequence 489 BP; 125 A; 134 C; 87 G; 143 T;
 SQ

PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvill JD,
 PI Roberts Rapp L, Russell JC, Stroupe SD;
 DR WPI: 98-27224/24.
 PT Detecting BS106 gene products - useful for developing products for
 detecting, staging, preventing, treating or determining
 predisposition to e.g. breast cancer.
 PT Claim 1; Page 90; 114pp; English.
 PS BS106 is a breast tissue gene with which breast cancer and related
 CC diseases are associated. The BS106 polynucleotides V31989-V31993 can be
 CC detected by BS106 specific polynucleotides or complements acting as
 CC useful markers for detection methods. The products and methods can be
 CC used for detecting, diagnosing, staging, preventing or treating, or
 CC determining predisposition to diseases or conditions of the breast such
 CC as breast cancer.
 SQ Sequence 553 BP; 159 A; 144 C; 101 G; 148 T;

Query Match 1.2%; Score 17; DB 1; Length 553;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PI V29521 standard; cDNA: 732 BP.
 DR V29521; standard; cDNA: 732 BP.
 AC V29521; standard; cDNA: 732 BP.
 DT 13-Oct-1998 (first entry)
 DE Homo sapiens LexA-PS-1 fusion protein cDNA.
 KW Presenilin-1; LexA; PS-1; Presenilin-1; PSP-1;
 KW Alzheimer's disease; serine protease; neurodegeneration;
 KW Predisposition; diagnosis; ss.
 OS Homo sapiens.
 PH Location/Qualifiers 2..523
 FT CDS /**tag= a product= LexA-PS- fusion protein
 FT /product= LexA-PS- fusion protein
 FT PN EP-828003-02.
 PT Diagnosing pre-disposition to Alzheimer's disease, etc.
 PD 11-MAR-1998.
 PF 26-AUG-1997; 306501.
 PR 06-SEP-1996; US-025456.
 PR 25-OCT-1996; US-027813.
 PA (SMIK) SMITHKLINE BECHAM CORP.
 PA (SMIK) SMITHKLINE BECHAM PLC.
 PI Browne MJ, Clinkenbeard HE, Creasy CL, Karran EH,
 PI Livi GP, Southan CD;
 DR WPI: 98-161101/15.
 DR P-PSDB; W55766.
 PT Diagnosing pre-disposition to Alzheimer's disease, etc.
 PT Example 2; Page 17; 65pp; English.
 PS The sequence is that encoding a LexA-PS-1 fusion protein which
 CC was used in the cloning of PSP-1. This can be used to identify
 CC modulators of serine protease activity and also to diagnose a
 CC condition associated with lack of one of the serine proteases
 CC or a genetic predisposition to neurodegeneration in a patient,
 CC preferably PSP-1. This can be used to identify a genetic predisposition to Alzheimer's disease.
 SQ Sequence 732 BP; 197 A; 184 G; 174 T;

Query Match 1.2%; Score 17; DB 1; Length 732;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PI V31993/C standard; DNA; 553 BP.
 AC V31993;
 DT 25-SEP-1998 (first entry)
 DE BS106 polynucleotide clone 1662885 (1ii).
 KW ss: human; BS106; breast tissue gene; breast cancer; detection marker.
 OS Homo sapiens.
 PN W0818945-A1.
 PD 07-MAY-1998.
 PF 31-OCT-1997; U19886.
 PR 31-OCT-1996; US-742067.
 PA (ABBO) ABBOTT LAB.
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,

Query Match 1.2%; Score 17; DB 1; Length 836;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PI 820 atctctttgtccatccc 836
 DB 131 ATCTCCTTGCATCC 147

RESULT 12
 V28875/C
 ID V28875; standard; CDNA: 1029 BP.
 AC V28875;
 DT 28-AUG-1998 (first entry)
 DE Candida antarctica lipase B clb gene coding region.
 KW Host cell; neutral metalloprotease; alkaline protease; lipase B;
 KW clb gene; ss
 OS Candida antarctica.
 PN WO9812300-A1.
 PD 26-MAR-1998.
 PF 19-SEP-1997; DK0397.
 PR 19-SEP-1996; DK-001024.
 PA (NOVO) NOVO-NORDISK AS.
 PI Lehmbck J;
 DR WPI; 98-217244/19.
 PT New modified host cells - are modified to express reduced levels of
 metallo protease and alkaline protease, used to increase production
 of heterologous protein products
 PR 06-JUN-1997; US-048894.
 PS Example 2; Page 32; 49pp; English.
 CC This polynucleotide comprises the coding region of the lipase B
 clb gene of *Candida antarctica*. The clb gene was isolated from a
 C. antarctica genomic library using probes (see V28873-74) based on
 the N-terminal amino acid sequence (see W57238) of lipase B. The
 gene was expressed in *Aspergillus oryzae* IFO 4177 and IFO 228, the
 latter having both the alkaline protease alp gene (see V28870) and
 neutral metalloprotease I npi gene (see V28869) deleted. CLB
 activity reached 1041 LU/g after 93 hr fermentation of IFO228,
 compared with 575 LU/g with IFO 4177. The invention provides
 metalloprotease- and alkaline protease-deleted yeast and fungal
 host cells and their use for improved production of heterologous
 protein products.
 Sequence 1029 BP; 183 A; 376 C; 259 G; 211 T;

Query Match	Best Local Similarity	Score	Length	DB	No.	Mismatches	Indels	Gaps	O;
Qy	58	ggctgcgaaaggcagg	74						
Db	110	GCTGGAAAAAGCAGG	94						

Sequence 1029 BP; 183 A; 376 C; 259 G; 211 T;

RESULT 13
 V84576/C
 ID V84576; standard; DNA: 1348 BP.
 AC V84576;
 DT 01-MAR-1999 (first entry)
 DE Human secreted protein gene 166 clone HCEQA68.
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
 developmental abnormality; foetal abnormality; blood; allergy; renal; ds;
 immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 osteoporosis; arthritis; testis; lung; thyroiditis; thyroditis; thymus; endocrine;
 metabolism; regulation; malabsorption; gastritis; neoplasms.
 OS Homo sapiens.
 PN WO984563-A2.
 PD 10-DEC-1998.
 PR 18-DEC-1997; U11422.
 PR 06-JUN-1997; US-070923.
 PR 06-JUN-1997; US-048877.
 PR 06-JUN-1997; US-048881.
 PR 06-JUN-1997; US-048884.
 PR 06-JUN-1997; US-048893.
 PR 06-JUN-1997; US-048896.
 PR 06-JUN-1997; US-048915.
 PR 06-JUN-1997; US-048949.
 PR 06-JUN-1997; US-048964.
 PR 06-JUN-1997; US-048972.

PR 06-JUN-1997; US-049020.
 PR 06-JUN-1997; US-049375.
 PR 05-SEP-1997; US-057638.
 PR 05-SEP-1997; US-057335.
 PR 05-SEP-1997; US-057644.
 PR 05-SEP-1997; US-057647.
 PR 05-SEP-1997; US-057550.
 PR 05-SEP-1997; US-057651.
 PR 05-SEP-1997; US-057667.
 PR 05-SEP-1997; US-057761.
 PR 05-SEP-1997; US-057764.
 PR 05-SEP-1997; US-057770.
 PR 05-SEP-1997; US-057775.
 PR 05-SEP-1997; US-057778.
 PR 06-JUN-1997; US-048875.
 PR 06-JUN-1997; US-048878.
 PR 06-JUN-1997; US-048882.
 PR 06-JUN-1997; US-048885.
 PR 06-JUN-1997; US-048894.
 PR 06-JUN-1997; US-048897.
 PR 06-JUN-1997; US-048940.
 PR 06-JUN-1997; US-048916.
 PR 06-JUN-1997; US-048962.
 PR 06-JUN-1997; US-048970.
 PR 06-JUN-1997; US-048974.
 PR 06-JUN-1997; US-049273.
 PR 05-SEP-1997; US-057584.
 PR 05-SEP-1997; US-057229.
 PR 05-SEP-1997; US-057642.
 PR 05-SEP-1997; US-057645.
 PR 05-SEP-1997; US-057648.
 PR 05-SEP-1997; US-057551.
 PR 05-SEP-1997; US-05762.
 PR 05-SEP-1997; US-05768.
 PR 05-SEP-1997; US-057762.
 PR 05-SEP-1997; US-057765.
 PR 05-SEP-1997; US-057771.
 PR 05-SEP-1997; US-057776.
 PR 06-JUN-1997; US-048876.
 PR 06-JUN-1997; US-048880.
 PR 06-JUN-1997; US-048883.
 PR 06-JUN-1997; US-048889.
 PR 06-JUN-1997; US-048895.
 PR 06-JUN-1997; US-048898.
 PR 06-JUN-1997; US-048901.
 PR 06-JUN-1997; US-048963.
 PR 06-JUN-1997; US-048911.
 PR 06-JUN-1997; US-049019.
 PR 05-SEP-1997; US-049374.
 PR 05-SEP-1997; US-057634.
 PR 05-SEP-1997; US-057443.
 PR 05-SEP-1997; US-057646.
 PR 05-SEP-1997; US-057649.
 PR 05-SEP-1997; US-057554.
 PR 05-SEP-1997; US-057566.
 PR 05-SEP-1997; US-057760.
 PR 05-SEP-1997; US-057763.
 PR 05-SEP-1997; US-057774.
 PR 05-SEP-1997; US-057777.
 PR (HUMAN) HUMAN GENOME SCI. INC., Ebner R, Endress GA,
 PI Brewer LA, Carter KC, Dillon PJ, Fischer CL, Florence C,
 PI Fan P, Feng P, Ferrile AM, Hu J, Kyaw H, Lafleur DW,
 PI Florence K, Greene JM, Olsen HS, Rosen CA, Ruben SM,
 PI Li Y, Moore PA, Ni J, Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
 PI WPI: 99-059865/05.
 DR P-PSDB; W88699.
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders

Claim 4: Page 427-428; 772PP; English.
The invention relates to nucleic acid sequences ('V84411 to V84633') encoding human secreted proteins (W88534 to W88756). The secreted protein gene sequences are deposited with the ATCC under deposit numbers ATCC 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010, 209011, 209012, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, tumours, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, restenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The present sequence represents a gene encoding a human secreted protein.

Query Match Similarity 1.2%; Score 17; DB 1; Length 1348;
 Best Local Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps

RESULT	14
29523	V29523 standard; cDNA: 1503 bp.
V29523;	
AC	V29523;
DT	13-OCT-1998 (first entry)
DE	Homo sapiens PSP1 clone.
KW	PS 1; presenilin; presenilin-1; PSP-1; Alzheimer's disease; serine protease; neurodegeneration; predisposition; diagnosis; ss.
DB	TGACCGCGGCCATCGTG 8

	Location/Qualifiers
Homo sapiens.	
Key	1..1272
CDS	/*tag= a transluc= pcDNA fractm=
OOS	
FFH	
CFFT	
FTT	

EP-828003-A2.

111-MAR-1998; 306501.
226-AUG-1997; 3032875.
113-DEC-1996; US-032875.
006-SEP-1996; US-02536.
225-OCT-1996; US-02773.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
Brown MJ, Clinkenbeard HE, Creasy CL, Karra
Livi GP, Southan CD;

WP1; 96-10101/13.
 DR P-PDB: W56788.
 DR Nucleic acids encoding human serum protease protein(s) - used for
 PT diagnosing pre-disposition to Alzheimer's disease, etc.
 PT Example 2; Page 19-20; 65pp; English.
 PS The sequence is that of an isolated cDNA clone encoding at least
 CC part of the serine protease PSP1. This can be used to identify
 CC modulators of serine protease activity and also to diagnose a
 CC condition associated with lack of one of the serine proteases
 CC or a genetic predisposition to neurodegeneration in a patient,
 CC preferentially predisposition to Alzheimer's disease.
 CC Sequence 1503 BP; 329 A; 405 C; 448 G;
 SO 321 T;

Search completed: April 14, 2000, 18:30:14
Total time: 5955 sec

Query Match	Score	DB 1	Length	1787;
Best Local Similarity	1.28;	Score 17;	DB 1;	
Matches 17;	Conservative	Pred. No. 37;	Mismatches	0;
QY	820	atcccttgcacatccc	Indels	0;
			Gaps	0;
Db	1048	ATCCCTTGCATCCC		



Result No.	Score	Query Match	Length	DB ID	Description
c 1	1.2	49377	2	US-08-764-233A-1	Sequence 1, Appli
c 2	1.1	76	6	PCT-US91-03942-77	Sequence 27, Appli
c 3	1.1	388	1	US-08-171-385-10	Sequence 10, Appli
c 4	1.1	894	2	US-08-534-910B-4	Sequence 4, Appli
c 5	1.1	929	5	US-08-860-368B-4	Sequence 19, Appli
c 6	1.1	1155	5	US-08-860-368B-19	Sequence 1, Appli
c 7	1.1	1158	5	US-08-860-368B-1	Sequence 4, Appli
c 8	1.1	1288	1	US-08-14-897-4	Sequence 68, Appli
c 9	1.1	1479	1	US-08-476-008-68	Sequence 68, Appli
c 10	1.1	1479	1	US-08-506-053-68	Sequence 68, Appli
c 11	1.1	1479	2	US-08-833-485-68	Sequence 9, Appli
c 12	1.1	2061	1	US-08-204-65B-9	Sequence 5, Appli
c 13	1.1	2061	1	US-08-170-702-5	Sequence 7, Appli
c 14	1.1	2061	1	US-08-467-831-5	Sequence 7, Appli
c 15	1.1	2157	3	US-08-132-990A-7	Sequence 7, Appli
c 16	1.1	2157	6	PCT-US92-0932A-7	Sequence 9, Appli
c 17	1.1	4474	1	US-08-480-547A-9	Sequence 9, Appli
c 18	1.1	4474	2	US-08-250-847A-9	Sequence 9, Appli
c 19	1.1	4474	4	US-08-463-949A-9	Sequence 20, Appli
c 20	1.1	4474	6	PCT-US94-06066-9	Sequence 20, Appli
c 21	1.1	5541	2	US-08-920-812-20	Sequence 20, Appli
c 22	1.1	5541	2	US-08-920-827-20	Sequence 20, Appli
c 23	1.1	5541	2	US-08-362-577C-20	Sequence 20, Appli
c 24	1.1	5541	3	US-08-920-828-20	Sequence 20, Appli
c 25	1.1	8378	6	PCT-US91-09055-1	Sequence 1, Appli
c 26	1.1	8378	6	PCT-US91-09055-1	Sequence 3, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution and is derived by analysis of the total score distribution.

SUMMARIES

DESCRIPTION

Result No.	Score	Query Match	Length	DB ID	Description
c 1	1.2	49377	2	US-08-764-233A-1	Sequence 1, Appli
c 2	1.1	76	6	PCT-US91-03942-77	Sequence 27, Appli
c 3	1.1	388	1	US-08-171-385-10	Sequence 10, Appli
c 4	1.1	894	2	US-08-534-910B-4	Sequence 4, Appli
c 5	1.1	929	5	US-08-860-368B-4	Sequence 19, Appli
c 6	1.1	1155	5	US-08-860-368B-19	Sequence 1, Appli
c 7	1.1	1158	5	US-08-860-368B-1	Sequence 4, Appli
c 8	1.1	1288	1	US-08-14-897-4	Sequence 68, Appli
c 9	1.1	1479	1	US-08-476-008-68	Sequence 68, Appli
c 10	1.1	1479	1	US-08-506-053-68	Sequence 68, Appli
c 11	1.1	1479	2	US-08-833-485-68	Sequence 9, Appli
c 12	1.1	2061	1	US-08-204-65B-9	Sequence 5, Appli
c 13	1.1	2061	1	US-08-170-702-5	Sequence 7, Appli
c 14	1.1	2061	1	US-08-467-831-5	Sequence 7, Appli
c 15	1.1	2157	3	US-08-132-990A-7	Sequence 7, Appli
c 16	1.1	2157	6	PCT-US92-0932A-7	Sequence 9, Appli
c 17	1.1	4474	1	US-08-480-547A-9	Sequence 9, Appli
c 18	1.1	4474	2	US-08-250-847A-9	Sequence 9, Appli
c 19	1.1	4474	4	US-08-463-949A-9	Sequence 20, Appli
c 20	1.1	4474	6	PCT-US94-06066-9	Sequence 20, Appli
c 21	1.1	5541	2	US-08-920-812-20	Sequence 20, Appli
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RESULT 1
 ; Sequence 1, Application US/08764233A
 ; Patent No. 5716849
 GENERAL INFORMATION:
 APPLICANT: Ligon, James M.
 APPLICANT: Schupp, Thomas
 APPLICANT: Beck, James J.
 APPLICANT: Beck, Dwight S.
 APPLICANT: Neff, Snezanna
 APPLICANT: Ryals, John A.
 TITLE OF INVENTION: Genes For the Biosynthesis Of Soraphen
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ciba-Geigy Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
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 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/258,261
 FILING DATE: 08-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Melgs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: 1506/CIP6
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (919) 541-8587
 INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4 9377 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Sorangium cellulosum
 IMMEDIATE SOURCE:
 IMMEDIATE SOURCE: CLINE: p98/1, pJL3, and pVKM15
 FEATURE:
 LOCATION: 383..760
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 to the reductase domains of type I PKS such as eryA from
 Saccharopolyspora erythraea."

FEATURE:
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 OTHER INFORMATION: /product= "Sora"
 /note= "Gene product is highly homologous to type I PKS
 involved in the synthesis of polyketide compounds."
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 OTHER INFORMATION: /product= "Module 1 of Sora"
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 OTHER INFORMATION: /product= "Module 2 of Sora"
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 OTHER INFORMATION: /product= "Module 3 of Sora"
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 OTHER INFORMATION: /product= "SorB"
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 NAME/KEY: misc_feature
 LOCATION: 13870..24556
 OTHER INFORMATION: /product= "Module 1 of SorB"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 24638..30820
 OTHER INFORMATION: /product= "Module 2 of SorB"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 35528..40114
 OTHER INFORMATION: /product= "Module 4 of SorB"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 30881..35446
 OTHER INFORMATION: /product= "Module 3 of SorB"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 40190..46318
 OTHER INFORMATION: /product= "Module 5 of SorB"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 46851..47891
 OTHER INFORMATION: /product= "SorM"
 /note= "The protein encoded by the sorM gene is highly
 homologous to the methyltransferase from Streptomyces
 hygroscopicus that is involved in the synthesis of the
 polyketide rapsamicin."
 US-08-764-233A-1

ALIGNMENTS

RESULT 1
 ; Sequence 1, Application US/08764233A
 ; Patent No. 5716849
 GENERAL INFORMATION:
 APPLICANT: Ligon, James M.
 APPLICANT: Schupp, Thomas
 APPLICANT: Beck, James J.
 APPLICANT: Beck, Dwight S.
 APPLICANT: Neff, Snezanna
 APPLICANT: Ryals, John A.
 TITLE OF INVENTION: Genes For the Biosynthesis Of Soraphen
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Ciba-Geigy Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08764233A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/258,261
 FILING DATE: 08-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Melgs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: 1506/CIP6
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 1:

Query Match 1.28; Score 17; DB 2; Length 49377;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

RESULT 2
PC-US91-02942-27/c
Sequence 27, Application PC/TUSS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
APPLICANT: ATHWAL, DILWET S
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterene, Kessler, Goldstein & Fox
STREET: 1245 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 1991.04.29
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0586600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: NUCLEAR ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US91-02942-27

Query Match Score 1.1%; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

RESULT 3
US-08-171-385-10/c
Sequence 10, Application US/08171385
PATENT NO. 5527684
GENERAL INFORMATION:
APPLICANT: MARY E. RUSSELL
APPLICANT: ULRICKE UTANS
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

Query Match Score 1.1%; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

RESULT 4
US-08-534-910B-4/C
Sequence 4, Application US/08534910B
PATENT NO. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuro
APPLICANT: OHNUKA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kozo
APPLICANT: KOYAMA, Taneitoshi
TITLE OF INVENTION: Mutated Farnesyl-diphosphate Synthase Capable Of Synthesizing Geranylgeranyldiphosphate And Gene Coding For
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B

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FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39, 048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-4

RESULT 5
Query Match 1.1%; Score 16; DB 2; Length 894;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 269 cggacccgcttgcga 284
Db 722 CCGACCCGCTTGCAGA 707

RESULT 6
Query Match 1.1%; Score 16; DB 5; Length 929;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 139 gacgcca gtcgtcaga 154
Db 780 GACGGCAGTCAGTA 795

RESULT 6
Query Match 1.1%; Score 16; DB 5; Length 929;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 139 gacgcca gtcgtcaga 154
Db 780 GACGGCAGTCAGTA 795

RESULT 6
Sequence 4, Application US/08860368B
Patent No. 6002072
GENERAL INFORMATION:
APPLICANT: McMaster, Russell J.
APPLICANT: Boesshore, Maury L.
APPLICANT: Tricoli, David M.
APPLICANT: Reynolds, John F.
APPLICANT: Carney, Kim J.
APPLICANT: Gonsalves, Dennis
TITLE OF INVENTION: Papaya Ringspot Virus Coat Protein Gene
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: Suite 4700
CITY: Chicago
STATE: IL
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,368B
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa L.
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0181US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
US-08-860-368B-19

Query Match 1.1%; Score 16; DB 5; Length 1155;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

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RESULT 7
 Qy 139 gacggcagtgcgtca 154
 Db 1006 GACGGCAGTGTCACTA 1021

Sequence 1, Application US/08860368B
 Patent No. 6002072
 GENERAL INFORMATION:
 APPLICANT: McMaster, Russell J.
 APPLICANT: Boesshore, Maury L.
 APPLICANT: Tricoli, David M.
 APPLICANT: Reynolds, John F.
 APPLICANT: Carney, Kim J.
 APPLICANT: Gonsalves, Dennis
 TITLE OF INVENTION: Papaya Ringspot Virus Coat Protein Gene
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
 STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
 STREET: Suite 4700
 CITY: Chicago
 STATE: IL
 COUNTRY: U.S.A.
 ZIP: 60601

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/860,368B
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/005,917
 FILING DATE: 15-JAN-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/740,375
 FILING DATE: 05-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Dunn, Tracy D.
 REGISTRATION NUMBER: 34,587
 REFERENCE/DOCKET NUMBER: 5490A-92-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1288 base pairs
 TYPE: nucleic acid
 STANDINGNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 53..691
 US-08-142-897-4

Query Match 1.1%; Score 16; DB 1; Length 1288;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 448 atcaaaggccgtcgctca 463
 Db 982 ATCAAAGTCCTGCTCA 997

RESULT 9
 US-08-476-008-61/c
 Sequence 68, Application US/08476008
 GENERAL INFORMATION:
 Patent No. 567061
 APPLICANT: Barry, Gerard F.
 APPLICANT: Kishore, Ganesh M.
 APPLICANT: Padette, Stephen R.
 APPLICANT: Stallings, William C.
 TITLE OF INVENTION: Glycosate Tolerant 5-Enolpyruvylshikimate-3-Phosphate Synthases
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
 STREET: 700 Chesterfield Village Parkway
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA

RESULT 8
 US-08-142-897-4
 Sequence 4, Application US/08142897
 Patent No. 5447852
 GENERAL INFORMATION:
 APPLICANT: Friedman, Jeffrey S.


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749, 611
; FILING DATE: 28-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576, 537
; FILING DATE: 31-AUG-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Jr., Dennis R.
; REGISTRATION NUMBER: 30, 914
; REFERENCE/DOCKET NUMBER: 38-21(15117)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6099
; TELEFAX: (314)737-6067
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1479 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107 .. 1438
; US-08-833-485-68

Query Match 1.1%; Score 16; DB 2; Length 1479;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;
Qy 481 accgcataactcatacg 496
Db 1299 ACCGCCAATCTACATCG 1284

RESULT 12
US-08-204-656B-9
; Sequence 9, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuo
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050

; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; LIBRARY: Library of chromosomal DNA from Bacillus
; macerans, PMAC, generated by treating chromosomal DNA from Bacillus
; IAM1243 with a restriction enzyme, and inserting and linking restric-
; fragments to pBR322
; LIBRARY:
; LIBRARY: IAM1243
; LIBRARY: fragments to pBR322
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2061
; OTHER INFORMATION: /note= "Nucleotides 1-2061
; correspond to nucleotides 82-2142 of the Bacillus macerans
; cyclomaltoextrin glucanotransferase structural gene"
; OTHER INFORMATION:
; OTHER INFORMATION:
; US-08-204-656B-9

Query Match 1.1%; Score 16; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;
Qy 1171 ggcaacggccggaggc 1186
Db 1825 GGCAAGGCCCGGAC 1840

RESULT 13
US-08-470-702-5
; Sequence 5, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/204, 656
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050

```

TELEX: 248345
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2061 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (synthetic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-470-702-5

Query Match 1.1%; Score 16; DB 1; Length 2061;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 16; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1171 9gcaacgcgcgagc 1186
 Db 1825 GGCAACGCCGCCAGC 1840

RESULT 15
 US-08-132-990A-7
 ; Sequence 7, Application US/08132990A
 ; Patent No. 5834589
 ; GENERAL INFORMATION:
 ; APPLICANT: MERUELLO, DANIEL
 ; APPLICANT: YOSHIMOTO, TAKAYUKI
 ; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08132990A
 FILING DATE: 07-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/084,729
 FILING DATE: 29-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/05569
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/899,075
 FILING DATE: 11-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/806,178
 FILING DATE: 13-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/627,950
 FILING DATE: 14-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: MISTOCK, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: B105-004-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 LENGTH: 2157 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 -NAME/KEY: CDS
 LOCATION: 148..2034
 US-08-132-990A-7

Query Match 1.1%; Score 16; DB 3; Length 2157;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 16; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

TELEX: 248345
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2061 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (synthetic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-467-831-5

QY 450 caaaatccctgctcaac 465
Db 156 CAAAGTCCCTGCTCAAC 171

Search completed: April 14, 2000, 18:27:45
Job time: 7077 sec



GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: April 14, 2000, 17:42:31 : Search time 1303.77 Seconds
 (without alignments)
 4039.862 Million cell updates/sec

Title:	US-09-388-090-3
Perfect score:	1395
Sequence:	tcaaggcggcaatcccaaata.....tcaaggcggcaatcccggtcaa 1.395
Scoring table:	OLIGO_NUC
Gapop	60.0
Gapext	60.0
Searched:	453834 seqs, 1887831982 residues
Word size :	0
Total number of hits satisfying chosen parameters:	9077268
Minimum DB seq length:	0
Maximum DB seq length:	1000000

Post-processing: Listing first 1000 summaries

Database : EST:*

1: em_est1:*

2: em_est2:*

3: em_est3:*

4: em_est4:*

5: em_est5:*

6: em_est6:*

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8: em_est8:*

9: em_est9:*

10: em_est10:*

11: em_est11:*

12: em_est12:*

13: em_est13:*

14: em_est14:*

15: em_est15:*

16: em_est16:*

17: em_est17:*

18: em_est18:*

19: em_est19:*

20: gb_est1:*

21: gb_est2:*

22: gb_est3:*

23: gb_est4:*

24: gb_est5:*

25: gb_est6:*

26: gb_est7:*

27: gb_est8:*

28: gb_est9:*

29: gb_est10:*

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31: gb_est12:*

32: gb_est13:*

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37: gb_est18:*

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39: gb_est20:*

40: gb_est21:*

41: gb_est22:*

42: gb_est23:*

43: gb_est24:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	20	1.4	200 27 C03492	C03492 C03492 Huma

2	20	1.4	304	40	AA958603	ua15607_r	AI443030	sa31a05_y	
3	20	1.4	329	44	AI324092	mho412.x	AW176044	OVO-Bt010	
4	20	1.4	445	34	AA415998	vh2510.r	AA85242	EST18891	
C	5	20	1.4	458	27	AA013893	mho412.r	AA362044	EST17177
C	6	20	1.4	482	33	AA447906	zx11b06.r	N77431	Yz31g08_r1.
C	7	20	1.4	557	44	AA322461	mho412.y	AI674135	wd08b02_x
C	8	19	1.4	354	37	AA672965	vna48b11.r	AW016622	UI-H-Bt0P
C	9	19	1.4	508	47	AI538510	tdd0706.x	AW050788	wz21e04_x
C	10	19	1.4	633	28	AA106132	mm20f05.r	AA104816	EST175940
C	11	18	1.3	63	51	AI756231	ea41d11.y	AI496576	sbl3e08_y
C	12	18	1.3	330	20	D37319	CELK04HXF	AA149456	sag3c10_y
C	13	18	1.3	360	24	D68430	CELK13LC4F	AI934811	wpp9h04_x
C	14	18	1.3	371	48	AI55708	mqr93b02.y	AI437993	sa334f01_y
C	15	18	1.3	420	29	AA140161	mqr93b02.y	AA095733	15643_sqq
C	16	18	1.3	423	45	AI372103	am7804.x	AA20704	zq19h07_r
C	17	18	1.3	438	103	AA0447358	mqr9b0006L	AA1437564	8336f06_y
C	18	18	1.3	462	29	AA159654	zo86510.r	AA365550	EST76403
C	19	18	1.3	469	88	AQ833281	LMAJEFV1..1	AI214640	qm12a01_x
C	20	18	1.3	471	89	AQ911814	LMAJEFV1..1	AI1008557	EST20308
C	21	18	1.3	488	91	AQ136002	HS-3055_B	AA920819	vj83a11_r
C	22	18	1.3	491	97	AQ216777	HS-3053_B	C13485	C1345_y
C	23	18	1.3	502	103	AA0449287	mqr9b0023K	C63387	C63387
C	24	18	1.3	551	21	T62818	yc70b04.s1	C65143	C65143
C	25	18	1.3	564	63	AQ947590	030304D11	AV186467	AV186467
C	26	18	1.3	597	100	AQ276833	CITB1-EI-	AV192074	AV192074
C	27	18	1.3	619	103	AQ469404	CITB1-EI-	AV198387	AV198387
C	28	18	1.3	645	42	AQ107025	GHO6310.3	AA326832	EST30067_B
C	29	18	1.3	668	104	AQ43740	RPC1-11-3	AI627199	ly94h01_x
C	30	18	1.3	693	104	AQ45949	CITB1-EI-	AA225545	ncb0b08_s
C	31	18	1.3	723	91	AQ158994	tdxb0012L	AI933675	wn42a10_x
C	32	18	1.3	756	34	AA519798	T9ES7zz35	AI626283	CITB1-EI-
C	33	18	1.3	756	91	AQ163302	mqr9x0023P	AI356408	ATB1-EI-
C	34	18	1.3	806	45	AQ136645	Qy16d12.x	AI980839	Pat_pk003
C	35	18	1.3	893	80	AF075974	Sa1mone11	AI27199	wh90c09_x
C	36	18	1.3	901	80	AF075966	Sa1mone11	AI008558	EST20309
C	37	18	1.3	973	80	AF075860	Sa1mone11	AI645916	vn11d12_r
C	38	18	1.3	977	80	AF075892	Sa1mone11	AI261749	QK10a03_x
C	39	18	1.3	1050	79	CNS00GGRM	AF072458	N25993	Yx88606..s1
C	40	18	1.3	1076	80	AF075862	Drosophil	AI45456	ab99b06_r
C	41	18	1.3	1089	28	UT0074	HSU0074_Hu	T45453	8716_Lambda
C	42	18	1.3	1101	79	CNS00120	AF0756113	AI24535	ATTS279_ve
C	43	17	1.2	73	40	AQ931149	o070-09..S	R75793	Y12109..rl
C	44	17	1.2	106	27	AA024642	2e73a05.r	AI016764	UI-H-Bt0P
C	45	17	1.2	117	42	AA024642	2e73a03.x	AI418060	AW028747
C	46	17	1.2	124	45	AI126325	QdB2e03..x	R36898	TF3f02_x
C	47	17	1.2	127	90	AQ025988	Qn02f10.x	AI71748	Yw32204..r1
C	48	17	1.2	127	90	AQ025988	EP(2)0380	AI244839	ui-R-Y..S
C	49	17	1.2	133	64	AW073768	xbl2g08..x	AI124048	qa94h04..S
C	50	17	1.2	135	47	AI196080	sqr5E03..y	AI636198	sd33e08..S
C	51	17	1.2	145	26	W85266	mf45h12..r1	AI67615	TEF0716..Y
C	52	17	1.2	148	60	AI794914	sb77e01.y	AA289213	wp35c06_r
C	53	17	1.2	151	74	AW225218	g7054C04	AI654973	LD01523..5
C	54	17	1.2	193	20	D1242	AI341610	AI909116	ol112a05_S
C	55	17	1.2	193	62	AI905624	CM-0T094-	AI250946	q13h10_x
C	56	17	1.2	211	63	AW009718	SB8610..x	AI580279	tm45f11..X
C	57	17	1.2	295	62	AI905837	IL-0T099..	AI71748	Yw32204..r1
C	58	17	1.2	258	46	AI141034	sqr5E08..y	AI0915	Y194f11..r1
C	59	17	1.2	286	31	AA302590	EST15812..y	AW100361	sd33e08..S
C	60	17	1.2	289	61	AI83248	at76607..x	AA67615	TEF0716..Y
C	61	17	1.2	290	32	AA341610	EST47198	AI67615	TEF0716..Y
C	62	17	1.2	294	32	AA340069	EST15219	AI289213	wp35c06_r
C	63	17	1.2	300	70	AV224407	AV224407	AI580279	tm45f11..X
C	64	17	1.2	296	32	AA366765	EST77750	AI07916	aw311d01..S
C	65	17	1.2	298	45	AI351243	gt47e05..x	AA135786	Z111f08..x
C	66	17	1.2	298	99	AQ013511	EP(2)2369	AA165795	fc18h12..y
C	67	17	1.2	299	50	AI572376	ty64e01..x	AI73235	Ys16f01..s1
C	68	17	1.2	300	21	F01731	HSC23EB071..N	AA092926	aa766295_sq
C	69	17	1.2	300	90	AQ073299	1..2110607	AA766295	aa766295_sq
C	70	17	1.2	303	59	AV094160	AV094160	AA135786	Z111f08..x
C	71	17	1.2	304	90	AQ05925	1..21K101	AA165795	fc18h12..y
C	72	17	1.2	308	62	AI905687	IL-T095-	AI73235	H73235_Ys16f01..s1
C	73	17	1.2	312	88	AA092926	m0611.seq	AA766295	aa766295_sq

c 148	426	39	AA8885212	am34c12.s	221	17	AA562784	v144g03.r
c 149	427	43	AI1244110	9958bb10.x	c 222	17	A0658b29	HS_5312_B
c 150	428	64	AI043343	DKFZPd44F	c 223	17	A1713193	UT_R-10-a
c 151	429	39	AA8266818	mr9e0e6.s	c 224	17	AQ148485	mgxb0020F
c 152	429	39	AA864625	0d45d04.s	c 225	17	A0787066	ob93aa05.s
c 153	430	43	A1305050	EST000015	c 226	17	AA636495	vr18e10.r
c 154	431	44	A1305050	W72838	c 227	17	AA719302	zh35b11.s
c 155	432	26	W72838	d5f912.s1	c 228	17	A1798182	wh43f05.x
c 156	433	40	AA28664	ora48t04.s	c 229	17	AQ25445	HS_3034_B
c 157	434	24	H78162	yu8bh10.r1	c 230	17	AW16753	xn5590.r.x
c 158	435	26	W72837	W7837_zd5f912.r1	c 231	17	AQ84057	LMAJFV1_L
c 159	436	63	AW006216	W293903.x	c 232	17	AQ376675	RPC1-11-1
c 160	436	74	AW192133	x181c08.x	c 233	17	AI591148	tw86a0.x
c 161	438	43	A1203418	AI10c02.s	c 234	17	AL081531	Arabidps
c 162	438	44	A1058424	ut7-R-Cl-k	c 235	17	AQ633921	HS_2171_B
c 163	440	41	A1058424	H1292334	c 236	17	AI10258	EST21147
c 164	442	44	A1292334	qm77b10.x	c 237	17	A743109	ny92f05.s
c 165	442	88	AQ849884	LMAJFV1_L	c 238	17	AI955196	wk31b04.x
c 166	443	42	A1127172	qb99qa08.x	c 239	17	AI37825	cc3h05.s
c 167	445	45	A1332427	q125d08.x	c 240	17	AQ85570	CPG189x
c 168	446	45	A1261769	qk10c02.x	c 241	17	AI023165	ow66c02.s
c 169	447	38	A1745977	qb18903.s	c 242	17	AW00110	wt09c05.s
c 170	447	39	AA822994	vr39d09.r	c 243	17	AQ655922	Sheard_D
c 171	448	42	A1141722	ot20a03.x	c 244	17	AV388115	AV388115
c 172	450	25	N62285	yz9b12.s1	c 245	17	AW043303	614026607
c 173	450	63	A1943549	AI1943549_B8CmmFZ24	c 246	17	AA24244	mw25c10.r
c 174	451	23	A1160779	qe49h04.s1	c 247	17	AI672891	we73qf6.x
c 175	455	42	A1088801	qb21d12.x	c 248	17	AQ633932	RPC1-11-4
c 176	455	45	A1351877	qd21904.x	c 249	17	AI17392	vh99h07.r
c 177	456	63	AW005143	ww80c03.x	c 250	17	AW17086	f132b02.y
c 178	457	62	A1920700	614026607	c 251	17	AI17939	EST23024
c 179	457	63	AW005152	ww80d02.x	c 252	17	AI179329	AW14122
c 180	458	27	A1162474	aub66g06.x	c 253	17	AA872875	oh57h01.s
c 181	458	63	A1961190	TgESTzz17	c 254	17	AA09900	zk87e0.s
c 182	458	63	A1351877	wh17e03.x	c 255	17	AA098827	zn45a05.r
c 183	459	39	AA160114	2086a10.r	c 256	17	AA660699	00588_MtR
c 184	459	39	AA24101	zv80c05.r	c 257	17	AL038359	DKFZP56L
c 185	459	41	A10622297	Gh01453.s5	c 258	17	AA79313	EST188810
c 186	460	46	A1406459	EST234745	c 259	17	AA045236	zk65gn3.s
c 187	462	48	A1558834	fg67a08.y	c 260	17	AA846530	aj56f05.s
c 188	463	60	A1802061	tx29h01.x	c 261	17	AW018930	fd61h05.y
c 189	467	60	A1796951	we25b10.x	c 262	17	AO638249	9227p111H
c 190	468	87	AQ805033	hs3-3083.s1	c 263	17	AO688158	nbxb009L
c 191	468	97	AQ757352	ah69c07.s	c 264	17	AA7755	EST22023
c 192	472	64	AW028011	wh61b09.x	c 265	17	B7755	T27B24TR_TA
c 193	472	99	AQ196276	RcC11..61	c 266	17	AA287833	nbxb0031M
c 194	474	48	A1545310	fb74b12.y	c 267	17	AQ611338	RPC19-D
c 195	475	48	A1566238	tct70a09.y	c 268	17	AA630331	nr57b07.s
c 196	476	39	AA822995	ws39c10.x	c 269	17	AO322052	dkfzp56L
c 197	476	100	AQ323168	FPC11..10	c 270	17	AO275421	ww74d08.s
c 198	478	102	AQ349756	FPC11..12	c 271	17	AI664723	TENG0684
c 199	479	35	AA583038	mr80e02.s	c 272	17	AI092271	oz97e05.x
c 200	480	33	A401428	2168903.y	c 273	17	AQ916509	nbeb005E
c 201	480	63	A1988559	sd04a07.y	c 274	17	AL031328	DKFZP56L
c 202	481	12	A1545228	tct70a09.y	c 275	17	AO322052	nbxb0087E
c 203	482	12	A1566238	vt08e07.y	c 281	17	AW015050	Odt-0097
c 204	483	39	AQ349756	vt08e07.r	c 282	17	AO29182	nbxb0042J
c 205	483	22	R42167	Yf9e01.s1	c 283	17	AA522522	n38qd02.s
c 206	484	46	A1417420	tg30907.x	c 284	17	AL053617	Drosophil
c 207	484	46	A1399464	NCP4G11T	c 285	17	AL051517	Drosophil
c 208	485	48	A1545243	ut7-R-C3..t	c 286	17	AL065338	Drosophil
c 209	492	34	A4469302	nc68f04.s	c 287	17	AQ89086	HS_4831-B
c 210	496	63	A1941514	618030B03	c 288	17	AO60567	Drosophil
c 211	496	46	A1417420	tg30907.x	c 289	16	AI203654	gf48e05.x
c 212	498	46	A1399464	Yf9e01.s1	c 290	16	AQ57047	RPC1-11-4
c 213	499	39	A8875459	V125H1.mt	c 291	16	AT18057	Vt90f12.r
c 214	502	39	A881220	W10c05..r	c 292	16	AW074095	xb07f03.x
c 215	502	100	AQ300812	HS_2217_B	c 293	16	R83937	Lambd
c 216	505	69	AW123020	ut7-M-BH2	c 294	16	AI203654	gf48e05.x
c 217	506	69	AW141797	EST29190	c 295	16	AQ581047	AQ581047
c 218	507	69	H50305	H50305	c 296	16	AT18057	Vt90f12.r
c 219	509	34	AA462995	vt70c04.r	c 297	16	AW074095	xb07f03.x
c 220	509	88	AQ8465560	LMAJFV1_L	c 298	16	R83937	15896 Lambd

294	16	1.1	188	26	W35479	139	Mouse_V	c	367	16	1.1	320	48	AI582808
295	16	1.1	193	103	AQ485008			c	368	16	1.1	104	RPCI-11-3	H829547 RPCI-11-3
c 296	16	1.1	195	59	AV093650			c	369	16	1.1	325	24	H8295
297	16	1.1	195	74	AW219755	EST302217		c	370	16	1.1	327	20	Z25652
298	16	1.1	200	42	AII149336	qc76h03.x		c	371	16	1.1	327	32	AA366349 EST77284
299	16	1.1	203	69	AV206555	AV206555		c	372	16	1.1	331	90	AQ031642 HS_2225-B
c 300	16	1.1	211	102	AQ403396	HS_225_B		c	373	16	1.1	333	90	AQ009196 CIT-HPP-2
301	16	1.1	213	31	N48947	YY7sd10.x		c	374	16	1.1	334	33	AA339011 LD03296.5
302	16	1.1	214	31	AA308893	EST179987		c	375	16	1.1	337	27	AA038448 m192807.r
303	16	1.1	216	50	AI708411	as97b12.x		c	376	16	1.1	337	60	AV119872
c 304	16	1.1	218	71	AV256058	AV256058		c	377	16	1.1	338	39	AA833189 ud02103.r
305	16	1.1	219	50	AV039895	AV039895		c	378	16	1.1	339	90	AQ070924 HS_2268-A
306	16	1.1	219	88	AQ846781	LMJXFV1..1		c	379	16	1.1	342	29	AA112321 JM004038.
c 307	16	1.1	220	61	AV155909	AV155909		c	380	16	1.1	345	34	C25163 C23363 Rice
308	16	1.1	220	59	AV067339	AV067339		c	381	16	1.1	345	82	AQ616784 HS_5496-B
c 309	16	1.1	235	70	AV241809	AV241809		c	382	16	1.1	347	40	AA951481 LD31957.5
c 310	16	1.1	237	39	AA885632	o132a10..S		c	383	16	1.1	347	62	AV188650 AV188650
c 311	16	1.1	241	63	AT946380	bs24f07.y		c	384	16	1.1	347	63	AI95870 bs17309.y
c 312	16	1.1	242	43	C99795	C99795 YAC		c	385	16	1.1	349	59	AV110322
c 313	16	1.1	242	74	AV380962	AV380962		c	386	16	1.1	349	71	B54075 CIT-HPP-20.1
c 308	16	1.1	243	20	T14448	SMEST0109.S		c	387	16	1.1	353	80	AA201832 LD03743.5
c 315	16	1.1	243	72	AV292919	AV292919		c	388	16	1.1	353	47	AI467932 tJ84c04.x
c 316	16	1.1	246	30	AA266274	mz63f05..r		c	389	16	1.1	355	21	R14564 YF83e10.r1
c 317	16	1.1	247	34	AA466846	ve92g09..r		c	390	16	1.1	356	33	AA391750 LD10801.5
c 318	16	1.1	249	74	AV76746	AV76746		c	391	16	1.1	357	88	AQ841300
c 319	16	1.1	250	48	AV338944	AV338944		c	392	16	1.1	357	91	AQ091904 HS_3014-B
c 320	16	1.1	254	48	AT572526	te38hb07..x		c	393	16	1.1	358	20	Z43619 HSC1HF091..n
c 321	16	1.1	254	71	AV323763	AV323763		c	394	16	1.1	358	23	H41215 YP67b11..s1
c 322	16	1.1	255	24	H91784	Yx03h09..s1		c	395	16	1.1	358	44	AI308725 SWOATCAP
c 323	16	1.1	258	29	AA127054	zn28f09..s		c	396	16	1.1	359	21	B76220 RP0111-14A1
c 324	16	1.1	259	59	AV095548	AV095548		c	397	16	1.1	360	36	C62190 C6190 Yuji1
c 325	16	1.1	262	28	C15514	Y501c12..r1		c	398	16	1.1	360	36	C66985 C65985 Yuji1
c 326	16	1.1	266	71	AV278197	AV278197		c	399	16	1.1	361	51	AI70952 Cn06502..y
c 327	16	1.1	266	71	AV292919	AV292919		c	400	16	1.1	362	33	AA419052 LD1391.5
c 328	16	1.1	267	100	AQ264612	CITBTI-1..-		c	401	16	1.1	362	43	AI220074 9984d10..x
c 329	16	1.1	269	59	AV082003	AV082003		c	402	16	1.1	363	21	T66808 Ya00a11..rl
c 330	16	1.1	271	34	AA4889615	aa33ch12..r		c	403	16	1.1	363	23	H4280 Y63d01..rl
c 331	16	1.1	272	71	AA772123	ai40c12..s		c	404	16	1.1	365	36	AA633273 ns04h10..r
c 332	16	1.1	273	73	AV341111	AV341111		c	405	16	1.1	365	79	FR009261 AL000547 F_rubrippe
c 333	16	1.1	274	36	C73800	C73800_R1ee		c	406	16	1.1	366	81	B50113 CIT978SK-4
c 334	16	1.1	277	51	AV052860	AV052860		c	407	16	1.1	372	21	T84502 Yd19f04..r1
c 335	16	1.1	278	71	AV268832	AV268832		c	408	16	1.1	372	45	AI392636 487013F10
c 336	16	1.1	279	38	AA772123	ai40c12..s		c	409	16	1.1	373	38	AA51038 LD20821.5
c 337	16	1.1	279	49	AV014484	AV014484		c	410	16	1.1	373	21	T93973 ye29a04..r1
c 338	16	1.1	279	50	AV039520	AV039520		c	411	16	1.1	373	46	AI48991 tfa3e08..x
c 339	16	1.1	280	82	AQ667091	HS_2107_A		c	412	16	1.1	373	62	AI98292 wp12a08..x
c 340	16	1.1	281	72	AV300420	AV300420		c	413	16	1.1	374	44	AI32383B mt66b10..x
c 341	16	1.1	282	62	AV177297	AV177297		c	414	16	1.1	374	61	AIB26245 wf32b10..x
c 342	16	1.1	284	29	AA127053	zn28f09..r		c	415	16	1.1	375	21	T93973 ye29a04..r1
c 343	16	1.1	284	39	AA882981	TBN5058		c	416	16	1.1	376	64	AI88249 ZN28..61409H12
c 344	16	1.1	284	61	AI856565	sb39a05..y		c	417	16	1.1	376	47	AI490102 EST24844.1
c 345	16	1.1	284	72	AV290599	AV290599		c	418	16	1.1	380	27	C0998 AI19143 ub20a19..r
c 346	16	1.1	285	23	R97430	Yq5j1h01..s1		c	419	16	1.1	381	100	AQ972279 HS_3051..A
c 347	16	1.1	286	62	AI874226	t_z63a05..x		c	420	16	1.1	381	100	AI084749 q08h11..x
c 348	16	1.1	287	72	AA162174	av89f03..y		c	421	16	1.1	382	62	AI88249 ZN28..61409H12
c 349	16	1.1	288	69	AV214615	AV214615		c	422	16	1.1	382	29	AI88249 ZN28..61409H12
c 350	16	1.1	290	60	AV139975	AV139975		c	423	16	1.1	386	21	R17722 RY31ba06..r1
c 351	16	1.1	293	60	AV119054	AV119054		c	424	16	1.1	386	43	AI135785 qe80e06..x
c 352	16	1.1	295	59	AV118445	AV118445		c	425	16	1.1	387	21	T80606 Yd23f01..s1
c 353	16	1.1	297	64	AV118938	AV118938		c	426	16	1.1	388	33	AA42642 zv59g10..x
c 354	16	1.1	297	64	AV089750	x07e12..x		c	427	16	1.1	388	42	AI084749 q08h11..x
c 355	16	1.1	301	48	AO055630	AO055630		c	428	16	1.1	388	81	B87719 Rp0111-30D1..A
c 356	16	1.1	303	79	CNS005Q	CNS005Q		c	429	16	1.1	389	47	AI494189 tii14f12..r
c 357	16	1.1	304	69	AI135710	UI-H-B1L-		c	430	16	1.1	389	64	AW017204 EST2776-2
c 358	16	1.1	304	81	B83478	RPC111-15C		c	431	16	1.1	389	72	AW163868 61409H12
c 359	16	1.1	304	81	AI091110	HS_3007_B		c	432	16	1.1	389	47	AI488400 EST246722
c 360	16	1.1	311	69	AV215348	AV215348		c	433	16	1.1	393	35	AA558848 LD18410..5
c 361	16	1.1	312	69	AA108911	EST179788		c	434	16	1.1	393	39	AA80139 LD23616..5
c 362	16	1.1	313	62	AI92825	AI92825		c	435	16	1.1	393	87	AI072752 HS_2019..B
c 363	16	1.1	314	41	AU007657	AU007657		c	436	16	1.1	393	99	AQ25351 HS_2055..A
c 364	16	1.1	315	40	AQ640238	927P1..F6		c	437	16	1.1	394	88	AQ84618 nbxb0080..r
c 365	16	1.1	317	87	AQ817113	HS_5281..A		c	438	16	1.1	398	34	AA42480 T077803..r
c 366	16	1.1	320	42	AI099654	AI099654		c	439	16	1.1	398	37	T43614 6877 Lambda

C 440	16	31	AA286767	ZS51d06_r	AII083728	gf19d03_x	
C 441	16	400	AT399304	NCV70TA313	AW201529	sf04c04	y
C 442	16	1.1	401	29	AA154765	HS_2037_B	
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c	789	16	AI108315	AI108315	c	862	15	AA587076	nn7791.5
c	790	16	AI438586	AI438586	c	863	15	B4480	HS-1060-A1-
c	791	16	AI156170	AI156170	c	864	15	AA371653	EST83490
c	792	16	AI061971	AI061971	c	865	15	AA252796	nig1a005.s
c	793	16	AI0658119	AI0658119	c	866	15	AF009494	sapi
c	794	16	AI0947841	AI0947841	c	867	15	AA416261	vf38f12.r
c	795	16	AI13715	AI13715	c	868	15	AA75098	ISM0135
c	796	16	AI324990	mgxb0020M	c	869	15	AA21567	2999f10.s
c	797	16	AI0513083.5	AI0513083.5	c	870	15	AA370779	vw05h08.r
c	798	16	AI0660590	AI0660590	c	871	15	N84754	J0112F.Huma
c	799	16	AI0780297	HS_3169_B	c	872	15	B22563	F15G6TR.IGF
c	800	16	AI383892	AI383892	c	873	15	AA73072	nz94b01.s
c	801	16	AI274409	mgxb0015K	c	874	15	R29356	F1-477D.22
c	802	16	AI735552	LD21503.5	c	875	15	AA684852	EST105576
c	803	16	AI200219	RPC11-45	c	876	15	AI1801	zehn2431
c	804	16	AI290794	qml3b05.x	c	877	15	AI664321	ue84e09.r

878	15	60	AV128111	AV128111		c 951	15	1.1	235	38	AA785898
	c 879	15	33	AA13420	AA13420	c 952	15	1.1	235	41	AI030049
	c 880	15	1.1	153	AV247421	c 953	15	1.1	235	70	AV241571
	c 881	15	1.1	154	AV247421	c 954	15	1.1	235	71	AV322180
	c 882	15	1.1	154	AI326950	c 955	15	1.1	236	30	AA269660
	c 883	15	1.1	164	mp39n08.x	c 956	15	1.1	236	47	AI518670
	c 884	15	1.1	165	AV066596	c 957	15	1.1	236	70	AV221640
	c 885	15	1.1	165	AV066596	c 958	15	1.1	236	70	AV249900
	c 886	15	1.1	166	mp39n09.y	c 959	15	1.1	236	71	AV282691
	c 887	15	1.1	166	X88272 H. sapiens D	c 960	15	1.1	237	51	N92959
	c 888	15	1.1	169	AA879833 vvv8103.r	c 961	15	1.1	237	73	AV343110
	c 889	15	1.1	169	AA980204 ub55905.s	c 962	15	1.1	238	63	AW01620
	c 890	15	1.1	172	AA1553056 UI-R-C2P-	c 963	15	1.1	238	69	AW135967
	c 891	15	1.1	173	AV300394 AV300394	c 964	15	1.1	239	72	AV293029
	c 892	15	1.1	175	D67416 CELK053C8F	c 965	15	1.1	239	73	AV345936
	c 893	15	1.1	177	AV32035 AV32035	c 966	15	1.1	240	51	AU074936
	c 894	15	1.1	178	AA283450 RTB218 HT	c 967	15	1.1	241	30	AA259442
	c 895	15	1.1	179	W18069 mb85d04.r1	c 968	15	1.1	241	49	AV021637
	c 896	15	1.1	180	AV078125	c 969	15	1.1	241	50	AI696041
	c 897	15	1.1	180	CNS00XET	c 970	15	1.1	241	69	AV211114
	c 898	15	1.1	181	AA645027 vs86e07	c 971	15	1.1	241	72	AV289073
	c 899	15	1.1	181	AV360303 AV360303	c 972	15	1.1	241	74	AV376305
	c 900	15	1.1	182	AA004317 AV004317	c 973	15	1.1	243	41	AI070571
	c 901	15	1.1	184	AI149168 qc76a11.x	c 974	15	1.1	243	72	AV057762
	c 902	15	1.1	184	AI516074 fbt77h01.y	c 975	15	1.1	243	73	AV351186
	c 903	15	1.1	185	AA094345 119455..se	c 976	15	1.1	244	51	AI713733
	c 904	15	1.1	186	AA124243 qj60020.x	c 977	15	1.1	244	62	AI131988
	c 905	15	1.1	187	AA164496 mv36c12.x	c 978	15	1.1	244	70	AV247006
	c 906	15	1.1	193	AV274950 AV274950	c 979	15	1.1	245	20	T37102
	c 907	15	1.1	195	D55376	c 980	15	1.1	245	71	AV256272
	c 908	15	1.1	195	FRO0515236	c 981	15	1.1	245	72	AV331343
	c 909	15	1.1	199	W78509 me85e01.r1	c 982	15	1.1	246	47	AI467449
	c 910	15	1.1	200	T57768	c 983	15	1.1	246	59	AV087596
	c 911	15	1.1	202	AI1242891 qb5le06.x	c 984	15	1.1	247	48	AI612307
	c 912	15	1.1	202	AI24957 AV124957	c 985	15	1.1	247	69	AW140154
	c 913	15	1.1	202	AV123450 AV123450	c 986	15	1.1	247	62	AV1887096
	c 914	15	1.1	204	AI673389 wf1806.x	c 987	15	1.1	248	73	AV343982
	c 915	15	1.1	205	AA119443 mp67f03.r	c 988	15	1.1	248	36	AA606767
	c 916	15	1.1	205	AA119443 mp67f03.r	c 989	15	1.1	249	28	AA059591
	c 917	15	1.1	213	AI157834 ue59a12.si	c 990	15	1.1	249	51	AV055075
	c 918	15	1.1	214	AI94423 bsl0c03.y	c 991	15	1.1	249	62	AI1887096
	c 919	15	1.1	216	AV123453	c 992	15	1.1	249	73	AV343982
	c 920	15	1.1	218	AA238425 mx92c12.r	c 993	15	1.1	250	43	D79515
	c 921	15	1.1	220	AA918855 O16le10.s	c 994	15	1.1	250	59	AI232607
	c 922	15	1.1	221	AA50366 v908e09.r	c 995	15	1.1	250	60	AV089696
	c 923	15	1.1	221	AI553692 tq44le06.x	c 996	15	1.1	250	61	AV135645
	c 924	15	1.1	222	AA60337 nr2le06.s	c 997	15	1.1	250	69	AI1824453
	c 925	15	1.1	222	AV257831 AV257831	c 998	15	1.1	251	69	AW115209
	c 926	15	1.1	223	AI153311 uc48c04.r	c 999	15	1.1	251	37	AA731056
	c 927	15	1.1	223	AI845963 UI-M-AP1-	c1000	15	1.1	251	64	AW056440
	c 928	15	1.1	224	F19320 HSPD0920.H						
	c 929	15	1.1	225	AA362336						
	c 930	15	1.1	225	AI175573						
	c 931	15	1.1	225	70 AV227465						
	c 932	15	1.1	225	102 A0415823						
	c 933	15	1.1	226	40 AA991274						
	c 934	15	1.1	226	73 AV368200						
	c 935	15	1.1	228	34 AA503723						
	c 936	15	1.1	228	73 AV375804						
	c 937	15	1.1	229	50 AI107775						
	c 938	15	1.1	229	60 AV142070						
	c 939	15	1.1	229	73 AV365316						
	c 940	15	1.1	230	25 N60303						
	c 941	15	1.1	232	50 AV08596						
	c 942	15	1.1	232	73 AV361760						
	c 943	15	1.1	232	73 AV372182						
	c 944	15	1.1	232	73 FR016825						
	c 945	15	1.1	233	34 AA474779						
	c 946	15	1.1	233	43 AI195386 ui11n10.r						
	c 947	15	1.1	233	73 AV355672						
	c 948	15	1.1	234	26 W32267						
	c 949	15	1.1	234	46 AI029083 UI-RCO1						
	c 950	15	1.1	234	59 AV113882 AV113882						
						RESULT	1				
						LOCUS	C03492	200 bp	mRNA	EST	30-JUL-1996
						DEFINITION	C03492	Human heart cDNA (YNakamura)	Homo sapiens	ORGANISM	Eukaryota; Primates; Catarrhini; Hominidae; Homo.
						ACCESSION	C03492	YNakamura	cdNA clone	KEYWORD	Tanakura, T., Ogiwara, A., Uchiyama, I., Takagi, T., Yazaki, Y. and
						VERSION	C03492.1	GI:1466743		REFERENCE	Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing
						SOURCE				AUTHORS	Genomics 35 (1), 231-235 (1996)
						ORGANISM				TITLE	JOURNAL

MEDLINE 96299762
 COMMENT On Oct 18, 1995 this sequence version replaced gi:10232268.
 Contact: Yusuke Nakamura
 Institute of Medical Science
 University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
 Tel: 03-5449-5372
 Fax: 03-5449-5433
 Email: Yusuke@ims.u-tokyo.ac.jp.
 Location/Qualifiers
 1. .200
 /organism="Homo sapiens"
 /db_xref="Taxon:9606"
 /clone="3NHC1609"
 /clone_lib="Human heart cDNA"
 /dev_stage="adult"
 /note="Organ: heart; normalized directionally cloned cDNA
 from adult heart"
 BASE COUNT 51 a 63 c 49 g 36 t 1 others
 ORIGIN

Query Match 1.4%; Score 20; DB 27; Length 200;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 817 9gcatctttggccatccc 836
 Db 123 GGCACTCTCTTGGCCATCCC 142

RESULT 2
 AA958603 LOCUS AA958603 304 bp mRNA EST 08-MAY-1998
 DEFINITION Soares mouse mammary gland NbMMG Mus musculus cDNA clone
 IMAGE:1346820 5', similar to TR:Q92743 NOVEL SERINE PROTEASE.
 ; mRNA sequence.
 AA958603
 AA958603_1 GI:3124833
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Mammalia;
 Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 304)
 AUTHORS Marr,M., Hillier,L., Allen,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Scheellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Jan 19, 1998 this sequence version replaced gi:2282401.
 Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:695612

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .304
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:441503"
 /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"

/clone_lib="Soares mouse mammary gland NbMMG"
 /sex="male"
 /tissue_type="mammary gland"
 /lab_host="DH10B"
 /note="Organ: mammary gland; Vector: pT7T3D-Pac
 (Pharmacia) with a modified polylinker; Site_1: Not I -
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 Oligo(dT) primer [5',
 TGTACCAATCTGAATGGAGCGCGATGGTTTTTTTTTTTTTTTTTT
 T 3'] ; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT7T3 vector.
 RNA provided by Dr. Minoru KO, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M.Fatima
 Bonaldo."
 Bento Soares and M.Fatima

BASE COUNT 68 a 95 c 80 g 61 t
 ORIGIN Query Match 1.4%; Score 20; DB 40; Length 304;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 817 9gcatctttggccatccc 836
 Db 239 GGCACTCTCCTTGCATCCC 258

RESULT 3
 AI324092 LOCUS AI324092 329 bp mRNA
 mhab12_x1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA
 DEFINITION clone IMAGE:441503 3', similar to TR:Q92743 NOVEL SERINE PROTEASE.
 PROTEASE: ; mRNA sequence.
 ACCESSION AI324092
 VERSION AI324092_1
 KEYWORDS GI:4058521
 EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Mammalia;
 Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 329)
 AUTHORS Marr,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Scheellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Jan 17, 1998 this sequence version replaced gi:2044727.
 Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:466839
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 Possible reversed clone: similarity on wrong strand
 Possible reversed clone: polyA not found
 High quality sequence stop: 325.
 FEATURES
 source Location/Qualifiers
 1. .329
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:441503"
 /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"

QY 817 ggcatcccttggccatccc 836
 Db 330 GGATCTCCTTGCCATCCC 311

RESULT 8
 LOCUS AI672965/c
 DEFINITION Barsted mouse myotubes MPLRB5 Mus musculus cDNA clone.
 IMAGE:1024413 5', mRNA sequence.
 ACCESSION AA672965
 VERSION AA672965.1
 KEYWORDS EST.
 ORGANISM Mus musculus
 SOURCE house mouse.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 354)
 AUTHORS Marra, M., Hillier, L., Allen, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Stepcoski, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HMM Mouse EST Project
 COMMENT Unpublished (1996)
 On Sep 12, 1996 this sequence version replaced gi:1393485.
 Contact: Marra M/Mouse EST Project
 WashU-HMM Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: moussest@wustl.edu
 This clone is available royalty free through LInL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:575189

SEQ PRIMER: -28m13 rev2 ET from Amersham
 High quality sequence stop: 342.
 Location/Qualifiers 1..354
 /organism="Mus musculus"
 /strain="C3H"
 /db_xref="taxon:10090"
 /clone_lib="Barstead mouse myotubes MPLRB5"
 /lab_host="DH10B"
 /note="Vector: pRTT3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand CDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTTCAGGATCTCAGGGAGGGGCCCTTTTTTTTTTTTTTT
 3]; double-stranded cDNA was ligated to Eco RI adaptors
 [AATTCCGATTCCTTG], digested with Not I and cloned into the
 Not I and Eco RI sites of the modified pRT3 vector.
 Library constructed by Bob Barstead. The C2C12 cell line
 (available from ATCC, catalog # CRL-1772) differentiates
 rapidly, forming contractile myotubes and producing
 characteristic muscle proteins.
 BASE COUNT 50 a 124 c 124 g 56 t
 ORIGIN

AI538510 LOCUS AI538510
 DEFINITION td0706.x1 NCI-CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2074978 3,
 similar to contains MSRI.t1 MSRI repetitive element ; mRNA
 sequence.
 ACCESSION AI538510
 VERSION AI538510.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metzoza; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 508)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Jun 5, 1998 this sequence replaced gi:3188259.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
 M.D., Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution found through the I.M.A.G.E. Consortium/LInL at:
 www.bio.llnl.gov/bbrp/Image.html

Insert Length: 817 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 487.
 Location/Qualifiers 1..508
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2074978"
 /Clone_11b="NCICGAP_CLL1"
 /tissue_type="B cell, chronic lymphocytic leukemia"
 /lab_host="DH10B"
 /note="Vector: pRTT3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTTCACCACTGAACTGAGGCCGCCTTTTTTTTTTTTTTT
 T 3]; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pRT3 vector.
 Library is normalized, and was constructed by Bento
 Soares and M.Fabima Bonaldo."
 BASE COUNT 81 a 192 c 129 g 115 t
 ORIGIN 1 others

Query Match 1.4% Score 19; DB 47; Length 508;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 19; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0; Gaps 0;

QY 217 ggcccccgcgcgcga 235
 Db 74 GGAGCCCCCGCCCCGGCGCA 56
 RESULT 9

Query Match 1.4% Score 19; DB 37; Length 354;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 19; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 217 ggcccccgcgcgcga 235
 Db 74 GGAGCCCCCGCCCCGGCGCA 56
 RESULT 10

LOCUS AA106132/C
 DEFINITION mm20f05.r1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA
 clone IMAGE:520815'; similar to Sw:SX14_MOUSE Q04892 SOX-14
 PROTEIN ; mRNA sequence.
 ACCESSION AA106132
 VERSION AA106132.1
 KEYWORDS EST.
 SOURCE house mouse.

/organism="Caenorhabditis elegans"						
/strain="CB1489 him-8(e1489)"						
/db_xref="taxon:6239"						
/clone_id="y43h10"						
/sex="hermaphrodite, male"						
/tissue_type="whole animal"						
/dev_stage="varied"						
BASE COUNT	125	a	56 c	54 g	95 t	
ORIGIN						
Query Match	1.3%	Score 18;	DB 20;	Length 330;		
Best Local Similarity	100.0%	Pred. No.	83;			
Matches	18;	Conservative	0;	Mismatches	0;	Gaps 0;
Qy	295	ttctacgaatttttcaaa	312			
Db	76	TTCATAGAAATTTCATAA	93			
RESULT	13					
LOCUS	D683.0					
DEFINITION	D68430	360 bp	mRNA	EST	07-DEC-1995	
ACCESSION	CEK131C4F	Yuiji Kohara unpublished	CDNA	Caenorhabditis elegans		
VERSION	D68430	clone YK131C4 5'	, mRNA	sequence.		
KEYWORDS	D68430..1	GI:1107152				
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
JOURNAL						
COMMENT						
FEATURES						
source						
Location/Qualifiers						
1.	.371					
tissue_type="heart"						
/organism="Mus musculus"						
/strain="NIH/Swiss"						
/note="Organ: heart; Vector: PBScript SK-"						
/db_xref="taxon:1090"						
/ECORI						
Site 2: XbaI; Cloned unidirectionally, Primer:						
Oligo dR: 93 pooled NIH/Swiss 13 day embryo hearts.						
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'						
/clone lib="Stratagene mouse heart (#937316)"						
/clone lib="Stratagene mouse heart (#937316)"						
/db_xref="pooled"						
/sex="pooled"						
/tissue_type="heart"						
/dev_stage="13 day embryo"						
/lab_host="SOLR (kanamycin resistant)"						
/note="Organ: heart; Vector: PBScript SK-"						
Site 1: EcoRI; Site 2: XbaI; Cloned unidirectionally, Primer:						
Oligo dR: 93 pooled NIH/Swiss 13 day embryo hearts.						
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'						
/clone sequence: 5' GAATTCCGACGGG 3' -3'						
/adaptor sequence: 5' CTCGAATTTTTTTTTTTT 3'						
/base_count 103 a	sequence: 5' CTCGAATTTTTTTTTTTT 3'	56 g	91 t			
ORIGIN						
Query Match	1.3%	Score 18;	DB 48;	Length 371;		
Best Local Similarity	100.0%	Pred. No.	85;			
Matches	18;	Conservative	0;	Mismatches	0;	Gaps 0;
Qy	1030	gacatcgccatgcgcctc	1047			
Db	252	GACATCGCCATGCCTC	269			
RESULT	15					
AA140161						
LOCUS	AA140161..1	420 bp	mRNA	EST	11-FEB-1997	
DEFINITION	mg93b02..r1	Stratagene mouse	heart	(#937316)		
PROTEIN	IMAGE:386251	5'-similar to	TR:G755748	G755748		
KEYWORD						
ORGANISM						
VERSION						
KEYWORD						
SOURCE						
Location/Qualifiers						
1.	.360					
/organism="Caenorhabditis elegans"						
/strain="CB1489 him-8(e1489)"						
/db_xref="taxon:6239"						
/clone_id="yki1ic"						
/tissue_type="whole animal"						
/dev_stage="varied"						
BASE COUNT	134	a	65 c	60 g	101 t	
ORIGIN						
Query Match	1.3%	Score 18;	DB 24;	Length 360;		
Best Local Similarity	100.0%	Pred. No.	84;			
Matches	18;	Conservative	0;	Mismatches	0;	Gaps 0;
Qy	295	ttctacgaatttttcaaa	312			
Db	128	TTCATAGAAATTTCATAA	145			
RESULT	14					
AA155707						
LOCUS	AA155707..1	420 bp	mRNA	EST	11-FEB-1997	
DEFINITION	mg93b02..r1	Stratagene mouse	heart	(#937316)		
PROTEIN	IMAGE:386251	5'-similar to	TR:G755748	G755748		
KEYWORD						
ORGANISM						
VERSION						
KEYWORD						
SOURCE						
Location/Qualifiers						
1.	.360					
/organism="Caenorhabditis elegans"						
/strain="CB1489 him-8(e1489)"						
/db_xref="taxon:6239"						
/clone_id="y43h10"						
/sex="hermaphrodite, male"						
/tissue_type="whole animal"						
/dev_stage="varied"						
BASE COUNT	125	a	56 c	54 g	95 t	
ORIGIN						
Query Match	1.3%	Score 18;	DB 20;	Length 330;		
Best Local Similarity	100.0%	Pred. No.	83;			
Matches	18;	Conservative	0;	Mismatches	0;	Gaps 0;
Qy	295	ttctacgaatttttcaaa	312			
Db	128	TTCATAGAAATTTCATAA	145			

ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus .
AUTHORS	1 (bases 1 to 420)
TITLE	The WashU-HMMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	On Sep 12, 1996 this sequence version replaced gi:1407398.
LOCATION	Contact: Marra M./Mouse EST Project
FEATURES	WASHU-HMMI Mouse EST Project
source	Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.wustl.edu
source	This clone is available royalty-free through LILN ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
source	Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 380.
source	Location/Qualifiers
source	1. .420
source	/organism="Mus musculus" /strain="NIH/Swiss" /db_xref=taxon:10090" /clone=IMAGI:586251" /clone_lib="Stratagene mouse heart (#937316)" /sex="pooled" /tissue_type="heart" /dev_stage="13 day embryos" /lab_host="SOJR (Kanamycin resistant)" /note="Organ: heart; Vector: pBluescript SK; Site:1: ECORI; Site:2: XbaI; Cloned unidirectionally. Primer: Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts; Average insert size: 1.0 kb; Uni-TAP XR vector; -5'; adaptor sequence: 5' GAATTCGGCAGCGG 3' -3'; adaptor sequence: 5' CTCGATTTTTTTTTTTTTTTTTTTTT 3' "
BASE COUNT	121 a 131 c 65 g 103 t
OPTION	

Quarry Match 179

Best Local Similarity 100.0%; Score 18; DB 29; Length 420; Pred. No. 86; Mismatches 0; Indels 0; Gaps 0.

Search completed: April 14, 2000, 17:43:40

